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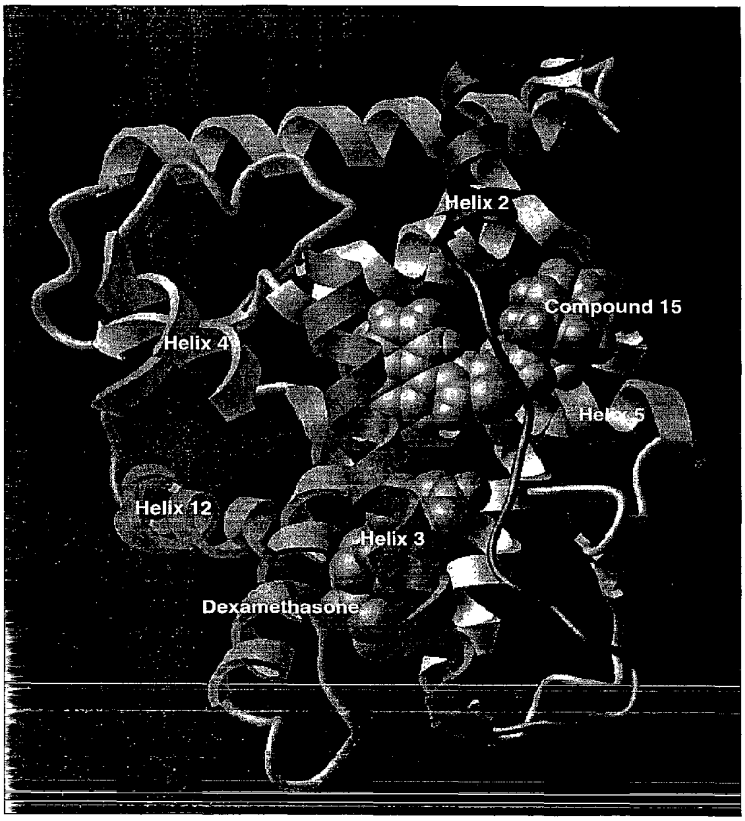
(54) Title: COMPOSITIONS AND METHODS INVOLVING NUCLEAR HORMONE RECEPTOR SITE II



(57) Abstract: A binding site in nuclear hormone receptors is described and its structural coordinates are provided. The invention provides machine-readable data storage media comprising structure coordinates of Site II and computer systems comprising the machine-readable data storage media. The invention provides methods used in the design and identification of ligands of Site II and of modulators of nuclear hormone receptors. The invention provides ligands of Site II, modulators of NHRs, pharmaceutical compositions comprising modulators of NHRs, methods of modulating NHRs, and methods of treating diseases by administering modulators of an NHR. Also provided are methods of designing mutants, mutant NHRs, Site II binding assays, and models of Site II.

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COMPOSITIONS AND METHODS INVOLVING NUCLEAR HORMONE RECEPTOR SITE II

This invention claims priority from provisional U.S. application Serial No. 60/396,907, filed July 18, 2002, which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The present invention generally relates to a binding site, termed Site II, in nuclear hormone receptors. The present invention relates to: machine-readable data storage media comprising structure coordinates of Site II; computer systems capable of producing three-dimensional representations of all or any part of Site II; methods used in the design and identification of ligands of Site II and of modulators of nuclear hormone receptors (NHRs); ligands of Site II; modulators of NHRs; methods of modulating NHRs; pharmaceutical compositions comprising modulators of NHRs; methods of treating diseases by administering modulators of an NHR; methods of designing mutants; mutant NHRs or portions of mutant NHRs; methods of measuring the binding of a test molecule to Site II; and models of Site II.

BACKGROUND OF THE INVENTION

The nuclear hormone receptor (NHR) family of transcription factors bind low molecular weight ligands and either stimulate or repress transcription. (in The Nuclear Receptor Facts Book, V. Laudet and H. Gronemeyer, Academic Press, p345, 2002). NHRs stimulate transcription by binding to DNA and inducing transcription of specific genes. NHRs may also stimulate transcription by not binding to DNA itself, rather they may modulate the activity of other DNA binding proteins (Stocklin, E., et al., Nature (1996) 383:726-8). The process of stimulation of transcription is called transactivation. NHRs repress transcription by interacting with other transcription factors or coactivators and inhibiting the ability of these other transcription factors or coactivators to induce transcription of specific genes. The process of repression of transcription is called transrepression. (for a review see The Nuclear Receptor Factsbook, V. Laudet and H. Gronemeyer, Academic Press, p42, 2002). For example, the glucocorticoid receptor, estrogen receptor, androgen

receptor and peroxisome proliferator activated receptors α and γ have been shown to repress the activity of the transcription factors AP-1 and NF-κB (Jonat, C., et al., Cell, 62, p1189-1204, (1990) Kallio, P.J., et al., Mol. Endocrinol., 9, p1017-1028 (1995), Keller, E.T., et al., J. Biol. Chem., 271, p26267-26275 (1996), Jones, D.C., et al., J. Biol. Chem., 277 (9), p6838-6845, (2002), Ricote, M., et al., Nature, 391, p79-82, (1998), Valentine, J.E., et al, J. Biol. Chem., 275, p25322-25329, (2000).

The nuclear hormone receptor family includes the glucocorticoid receptor (Hollenberg, S.M. et al.(1985) Nature, 318, p635), progesterone receptor (Misrahi, M. et al. (1987) Biochem. Biophys. Res. Commun. 143, p740), androgen receptor (Lubahn D. B., et al (1988), estrogen receptors (Green, S., et al. (1986) Nature 320, p134), mineralocorticoid receptor (Arriza, J.L., et al., (1987) Science 237, p268), retinoid receptors (RXRs and RARs) (Mangelsdorf, et al. (1990) Nature, 345, p224 and Petkovich M., et al (1987) Nature 330, p444), Vitamin D receptor, thyroid receptor (TR) (Nakai, A. et al., (1988) Mol. Endocrinol. 2, p1087), peroxisome proliferator activated receptor (PPAR) (Greene, M.E., et al. (1995) Gene Expression 4, p281), orphan nuclear receptors and others. Glucocorticoid receptor, progesterone receptor, androgen receptor, estrogen receptor, and mineralocorticoid receptor are steroid hormone receptors (SHRs).

Although the sequences vary amongst the various nuclear hormone receptors, they can be divided into functional domains including an N-terminal transactivation domain, a central DNA binding domain and a C-terminal ligand and dimerization domain. The ligands which bind these receptors act in a ligand, cell type, and promoter dependent fashion and include: glucocorticoids, progestins, retinoids, mineralocorticoids, and others. In addition to steroids, recent studies have shown that non-steroids can bind to nuclear hormone receptors and induce a biologic response (Coghlan, MJ, et al, J. Med. Chem. 44, p2879, 2001). Ligand cross-talk can occur between the receptors, for example, progesterone can bind not only the progesterone receptor but the glucocorticoid receptor as well (Zhang, S., Mol. Endocrinology 10, p24, 1996).

Three-dimensional structures of some of the nuclear hormone receptors have been elucidated through crystallization or homology modeling. A homology model

of the glucocorticoid receptor is disclosed in WO 00/52050, published September 8, 2000.

Recent publications by the same research group: Bledsoe, et. al., Cell, online publication by Cell Press, July 1, 2002, DOI: 10.1016/S0092867402008176; Cell, Vol 110, 93-105, 12 July 2002; and Apolito, et. al., in WO 03/015692 A2, published February 27, 2003; describe the successful crystallization and xray structural elucidation of the glucocorticoid receptor LBD as the dimer. X-ray structure coordinates were provided in WO 03/015692. Disruption of the dimeric structure was found to occur upon mutation of selected residues at the dimerization interface. Despite structural similarity to other steroid receptors, the GR LBD dimer represents a unique dimer configuration. The GR LBD used for this crystalization was a mutant (F602S) designed to provide a more soluble LBD construct.

Also recently, Kauppi et. al. published the stucture of the GR LBD bound to an antagonist, RU-486, in: the Journal of Biological Chemistry Online, JBC Papers In Press as DOI:10.1074/JBC.M212711200, April 9, 2003; and in J. Biol. Chem., Vol. 278, Issue 25, 22748-22754, June 20, 2003. In this structure, the GR LBD exhibits a significant displacement of helix 12, typical of antagonist action. In addition to the antagonist-bound LBD, a dimer structure similar to that reported by Bledsoe, et. al. was also described. The structure of the GR LBD – RU-486 complex was deposited in with the RCSB (1nhz.pdb)

Three dimensional structures of other nuclear hormone receptors are disclosed as follows, with RCSB (Research Collaboratory for Structural Bioinformatics, pdb file format) references in parentheses: RXRalpha (1lbd) Bourguet, W., Ruff, M., Chambon, P., Gronemeyer, H., Moras, D. Nature 375 pp. 377 (1995); PPAR-gamma (2prg) Nolte, R. T., Wisely, G. B., Westin, S., Cobb, J. E., Lambert, M. H., Kurokawa, R., Rosenfeld, M. G., Willson, T. M., Glass, C. K., Milburn, M. V. Nature 395 pp. 137 (1998); RARgamma (2lbd) Renaud, J. P., Rochel, N., Ruff, M., Vivat, V., Chambon, P., Gronemeyer, H., Moras, D. Nature 378 pp. 681 (1995); PR (1a28) Williams, S. P., Sigler, P. B. Nature 393 pp. 392 (1998); VitDR (1db1) Rochel, N., Wurtz, J. M., Mitschler, A., Klaholz, B., Moras, D. Mol. Cell 5 pp. 173 (2000); AR (1e3g) Matias, P. M., Donner, P., Coelho, R., Thomaz, M., Peixoto, C., Macedo, S., Otto, N., Joschko, S., Scholz, P., Wegg, A., Basler, S., Schafer, M., Egner, U.,

Carrondo, M. A. J.Biol.Chem. 275 pp. 26164 (2000); ERalpha (1a52) Tanenbaum, D. M., Wang, Y., Williams, S. P., Sigler, P. B. Proc Natl Acad Sci U S A 95 pp. 5998 (1998); ERbeta (112j) Shiau, A. K., Barstad, D., Radek, J. T., Meyers, M. J., Nettles, K. W., Katzenellenbogen, B. S., Katzenellenbogen, J. A., Agard, D. A., Greene, G. L. Nat.Struct.Biol. 9 pp. 359 (2002). It is generally thought that all steroid ligands bind to nuclear hormone receptors at the classical ligand binding site, which we term site I (Evans, RM. Science 240, p889, 1988). Limited proteolysis studies and cell transfection/mutagenesis studies have delineated the functional domains of nuclear hormone receptors which include a DNA binding domain, ligand binding domain and a transactivation domain. These studies provided the evidence that hormones bind to the ligand binding domain. Mutagenesis of GR has defined the dexamethasone interacting surface, defined as Site I, which includes amino acids Met-560, Met-639, Gln-642 and Thr-739 (Lind, U., et al. J. Biol. Chem. 275, p19041, 2000).

Recently, a second ligand binding site in ER-α and ER-β has been reported based on computational analysis and docking experiments with steroids. (van Horn, W. J. Med. Chem. 45, p584, 2002). This second binding site is not completely delineated. It is reported to have no obvious function, to be an evolutionary remnant, and to be absent in other nuclear receptors such as RARγ. Furthermore, there is no discussion of transrepression whatsoever. In addition, Endocrine Society Meeting June 2003, presentation OR34-1, Wang, Y., Chirgadze, NY, Briggs, SL, Khan, S., Jensen, EV., Burris, TP., A second binding site for hydroxytamoxifen with the ligand binding domain of estrogen receptor beta, describes the crystal structure of estrogen receptor bound with 4-hydroxytamoxifen, in which the ligand is found in two locations: the usual steroid binding pocket and a second site located along the hydrophobic groove near the cofactor binding region. This second site is remote from the Site II location described in this application.

The glucocorticoid receptor (GR) is a member of the nuclear hormone receptor family of transcription factors, and a member of the steroid hormone family of transcription factors. Affinity labeling of the glucocorticoid receptor protein allowed the production of antibodies against the receptor which facilitated cloning the human (Weinberger, et al. Science 228, p740-742, 1985, Weinberger, et al. Nature, 318, P635-641, 1985) and rat (Miesfeld, R. Nature, 312, p779-781, 1985)

glucocorticoid receptors. Subsequently, glucocorticoid receptors from other species were cloned including mouse (Danielson, M. et al. EMBO J., 5, 2513), sheep (Yang, K., et al. J. Mol. Endocrinol. 8, p173-180, 1992), and marmoset (Brandon, D.D., et al, J. Mol. Endocrinol. 7, p89-96, 1991). There is also a C-terminally distinct isoform of GR termed GR-beta. This isoform is identical to GR up to amino acid 727 and then diverges in the last C-terminal 15 amino acids. GR-beta is not known to bind glucocorticoids, is unable to transactivate, but does bind DNA (Hollenberg, SM. et al. Nature, 318, p635, 1985, Bamberger, C.M. et al. J. Clin Invest. 95, p2435, 1995). It is possible that GR-beta binds compounds other than the typical glucocorticoids.

Glucocorticoids which interact with GR have been used for over 50 years to treat inflammatory diseases. It has been clearly shown that glucocorticoids exert their anti-inflammatory activity via the inhibition by GR of the transcription factors NF-κB and AP-1. This inhibition is termed transrepression. It has been shown that the primary mechanism for inhibition of these transcription factors by GR is via a direct physical interaction. This interaction alters the transcription factor complex and inhibits the ability of NF-κB and AP-1 to stimulate transcription (Jonat, C., et al. Cell, 62, p1189, 1990, Yang-Yen, H.F., et al. Cell 62, p1205, 1990, Diamond, M.I. et al. Science 249, p1266, 1990, Caldenhoven, E. et al., Mol. Endocrinol. 9, p401, 1995). Other mechanisms such as sequestration of co-activators by GR have also been proposed (Kamer Y, et al., Cell 85, p403, 1996, Chakravarti, D. et al., Nature 383, p99, 1996). NF-κB and AP-1 play key roles in the initiation and perpetuation of inflammatory and immunological disorders (Baldwin, AS, Journal of Clin. Investigation 107, p3, 2001, Firestein, G.S., and Manning, A.M. Arthritis and Rheumatism, 42, p609, 1999, Peltz, G., Curr. Opin, in Biotech. 8, p467, 1997). NF-κB and AP-1 are involved in regulating the expression of a number of important inflammatory and immunomodulatory genes including: TNF-alpha, IL-1, IL-2, IL-5, adhesion molecules (such as E-selectin), chemokines (such as Eoxtaxin and Rantes), Cox-2, and others.

Although glucocorticoids are very effective anti-inflammatory agents, their systemic use is limited by their side effects which include diabetes, osteoporosis, glaucoma, Cushingoid syndrome, muscle loss, facial swelling, personality changes,

and others. (Stanbury, RM, and Graham, EM, Br. J. Opthalmology 82, p704, 1998, Da Silva, JAP., Bijlsma, J. Rheumatic Disease Clinics of North America, 26, p859, 2000)

In addition to leading to transrepression, the interaction of a glucocorticoid with GR can lead to stimulation by GR of transcription of certain genes. This stimulation of transcription is termed transactivation. Transactivation requires dimerization of GR and binding to a glucocorticoid response element (GRE). DNA binding is mediated via Zn fingers in the DNA binding domain (Giguere, V. et al Cell 46, p645, 1986; Rusconi, S. and Yamamoto, K.R. EMBO J., 6, p1309, 1987). DNA sequence specific interactions are determined by the C-terminal part of the first Zn finger (Danielsen, M., et al. Cell 57, p1131, 1989). Several GR target genes have been identified including MMTV, metallothionein, and tyrosine amino transferase (Ringold, GM et al, Cell 6, p299,1975; Scheidereit, C., et al Nature, 304, p749, 1983; Hager, LJ, Palmiter RD, Nature 291, 340, 1981; Grange, T., et al. Oncogene, 20, p3028, 2001). Transrepression, as opposed to transactivation, can occur in the absence of dimerization, and as mentioned above is believed to involve the direct interaction of GR with AP-1 and NF-κB.

Recent studies using a transgenic GR dimerization defective mouse which cannot bind DNA have shown that the transactivation (DNA binding) activities of GR could be separated from the transrepressive (non-DNA binding) effect of GR. These studies also indicate that many of the side effects of glucocorticoid therapy are due to the ability of GR to induce transcription of various genes involved in metabolism, whereas, transrepression, which does not require DNA binding leads to suppression of inflammation. (Tuckermann, J. et al. Cell 93, p531, 1998; Reichardt, HM. EMBO J., 20, p7168, 2001).

Compounds which can induce transrepression of GR with none to minimal induction of transactivation have been termed "dissociated steroids" (Vayassiere, BM, et al., Mol. Endocrinology, 11, p1249, 1997). Such "dissociated" compounds would be useful to treat inflammatory diseases. See Figure 1 for a graphical description of transactivation mediated by GR dimers versus transrepression mediated by GR monomers. It is possible that these "dissociated" compounds bind to GR without inducing dimerization yet allow the monomer to transrepress AP-1

and NF-κB. Another plausible explanation is that "dissociated" compounds may alter the conformation of GR to enable transrepression without inducing a DNA binding conformation.

There are several examples in the literature of compounds that possess dissociated activity as defined by the ratio of the effective concentration required to induce DNA binding in a cellular assay relative to the effective concentration required to transrepress, or inhibit AP-1 or NF-κB activity. The first report of a "dissociated steroid" published by Vayssiere, et al. Molecular Endocrinology, 11, p1245, 1997, showed that a derivative of dexamethasone had potent in vitro and in vivo anti-inflammatory activity with minimal induction of DNA binding. Subsequent studies (Coghlan, MJ, et al., J. Med. Chem. 44, p4481, 2001) have shown that non-steroidal compounds can bind to GR and elicit transrepressive activity with moderate transactivation activity. It is believed that each of the compounds described above act via the dexamethasone binding site.

Ursodeoxycholic acid (UDCA) has recently been shown to repress NF-κB activity via a GR mediated pathway. The compound appears to be "dissociated" as it does not induce DNA binding in a cellular assay. This compound, although acting in a GR dependent fashion, does not compete for dexamethasone binding to GR. Although direct binding of UDCA to GR has not been demonstrated, mutagenesis studies suggest that the ligand binding domain (LBD) of GR is required for activity. (Miura, T., J. Biol. Chem. 276, p47371, 2001). However, these studies did not delineate the specific amino acids which are involved in UDCA activity.

The art is in need of modulators of NHRs. A modulator of an NHR may be useful in treating NHR-associated diseases, that is diseases associated with the expression products of genes whose transcription is stimulated or repressed by NHRs. For instance, the art is in need of modulators of NHR that induce inhibition of AP-1 and NF-κB, as such modulators would be useful in the treatment of inflammatory and immune associated diseases and disorders, such as osteoarthritis, rheumatoid arthritis, multiple sclerosis, asthma, inflammatory bowel disease, transplant rejection, and graft vs. host disease.

The art is in need of compounds that possess dissociated activity, as such compounds would be useful in treating inflammatory and immune associated

diseases and disorders without exhibiting unwanted side effects. For instance, in the case of GR, although glucocorticoids are potent anti-inflammatory agents, their systemic use is limited by side effects. A dissociated compound that retained the anti-inflammatory efficacy of glucocorticoids while minimizing the side effects such as diabetes, osteoporosis and glaucoma would be of great benefit to a very large number of patients with inflammatory diseases.

The art is in need of compounds that antagonize transactivation. For instance, in the case of GR, such compounds may be useful in treating metabolic diseases associated with increased levels of glucocorticoid, such as diabetes, osteoporosis and glaucoma.

The art is in need of compounds that induce transactivation. For instance, in the case of GR, such compounds may be useful in treating metabolic diseases associated with a deficiency in glucocorticoid. Such diseases include Addison's disease.

In order to design compounds that modulate an NHR in specific ways, one needs to understand how ligands bind to an NHR and modulate the activity of the NHR.

SUMMARY OF THE INVENTION

We have identified a second binding site in the ligand binding domain of nuclear hormone receptors (NHRs). We refer to this second binding site as Site II.

Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. Table I is located under the heading for Example 21.

Figure 2 shows the amino acids of Site II in various human NHRs. The structure coordinates of Site II in the NHRs of Figure 2 are given in Table III, located under the heading for Example 22. Two sets of xray structure coordinates of Site II in GR are given in Table IV, located under the heading for Example 23, and Table V,

located under the heading for Example 24. Figure 6 shows the amino acids of Site II in the GR of various species.

We have found that ligands of Site II modulate NHRs. Ligands of Site II induce transrepression. Ligands of Site II possess dissociated activity. Ligands of Site II antagonize transactivation.

The invention provides machine-readable data storage media comprising data storage material encoded with machine readable data comprising all or any part of the structure coordinates of Site II. The invention provides computer systems comprising the machine-readable data storage media of the invention capable of producing three-dimensional representations of all or any part of Site II.

The invention provides methods used in the design and identification of ligands of Site II and modulators of NHRs. The invention provides: methods of docking a test molecule into all or any part of the cavity circumscribed by Site II; methods comprising identifying structural and chemical features of all or any part of Site II; methods of designing a ligand of Site II comprising modeling all or any part of Site II and designing a chemical entity that has structural and chemical complementarity with all or any part of Site II; methods of evaluating the potential of a chemical entity to bind to all or any part of Site II; methods for identifying a modulator of an NHR; and methods for identifying a ligand of Site II.

The invention provides ligands of Site II. The invention provides modulators of NHRs.

The invention provides methods of modulating an NHR.

The invention provides pharmaceutical compositions comprising modulators of NHRs.

The invention provides methods of treating diseases by administering a modulator of an NHR. Such diseases include NHR-associated diseases, diseases associated with NHR transactivation, diseases associated with NHR transrepression, diseases associated with AP-1-dependent gene expression, diseases associated with NF-κB-dependent gene expression, inflammatory or immune associated diseases and disorders, diseases treatable by inducing NHR transrepression, and diseases treatable by antagonizing NHR transactivation.

The invention provides methods of designing mutants comprising mutating Site II by making an amino acid substitution, deletion or insertion, and the resultant mutant NHRs, or portions of mutant NHRs, comprising a mutation in Site II.

The invention provides methods of measuring the binding of a test molecule to Site II.

The invention provides models of Site II.

All documents referred to herein, including but not limited to U.S. patent applications, are incorporated herein by reference in their entirety.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Graphical description of transactivation mediated by GR dimers versus transrepression mediated by GR monomers.

Figure 2. Consensus alignments carried out using ICM (Molsoft LLC, La Jolla, CA) between human GR (glucocorticoid receptor) LBD and other human NHR LBDs, indicating by shading the residues of Site II, i.e. residues corresponding to residues of GR Site II. Dots are spaceholders and do not represent amino acids. Numbers refer to the first residue in each line, are specific for each NHR and are based on the full-length NHR. For the NHRs listed below, with the exception of GR and MR, structural data was obtained from the RCSB references listed below, and the numbering system in the RCSB references was used. For GR and MR, structural data was obtained by homology modeling using the literature references below, and the numbering system in those literature references was used. The RCSB references (in parentheses) and literature references for the various NHRs are as follows: RXRalpha (SEQ ID NO:3) (1lbd) Bourguet, W., Ruff, M., Chambon, P., Gronemeyer, H., Moras, D. Nature 375 pp. 377 (1995); PPAR-gamma (SEQ ID NO:4) (2prg) Nolte, R. T., Wisely, G. B., Westin, S., Cobb, J. E., Lambert, M. H., Kurokawa, R., Rosenfeld, M. G., Willson, T. M., Glass, C. K., Milburn, M. V. Nature 395 pp. 137 (1998); RARgamma (SEQ ID NO:5) (2lbd) Renaud, J. P., Rochel, N., Ruff, M., Vivat, V., Chambon, P., Gronemeyer, H., Moras, D. Nature 378 pp. 681 (1995); PR (SEQ ID NO:6) (1a28) Williams, S. P., Sigler, P. B. Nature 393 pp. 392 (1998); VitDR (SEQ ID NO:7) (1db1) Rochel, N., Wurtz, J. M., Mitschler, A., Klaholz, B.,

Moras, D. Mol. Cell 5 pp. 173 (2000); AR (SEQ ID NO:8) (1e3g) Matias, P. M., Donner, P., Coelho, R., Thomaz, M., Peixoto, C., Macedo, S., Otto, N., Joschko, S., Scholz, P., Wegg, A., Basler, S., Schafer, M., Egner, U., Carrondo, M. A. J.Biol.Chem. 275 pp. 26164 (2000); ERalpha (SEQ ID NO:9) (1a52) Tanenbaum, D. M., Wang, Y., Williams, S. P., Sigler, P. B. Proc Natl Acad Sci U S A 95 pp. 5998 (1998); ERbeta (SEQ ID NO:10) (1l2j) Shiau, A. K., Barstad, D., Radek, J. T., Meyers, M. J., Nettles, K. W., Katzenellenbogen, B. S., Katzenellenbogen, J. A., Agard, D. A., Greene, G. L. Nat.Struct.Biol. 9 pp. 359 (2002); TRbeta (SEQ ID NO:11) (1bsx) Wagner, R. L., Darimont, B. D., Apriletti, J. W., Stallcup, M. R., Kushner, P. J., Baxter, J. D., Fletterick, R. J., Yamamoto, K. R. Genes Dev. 12 pp. 3343 (1998). MR and GR structural data were obtained by homology modeling to PR using the sequences from the following references: GR (SEQ ID NO:12), PIR Accession Number QRHUGA, Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G.,Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M. Nature (1985) 318: 635-641; MR (SEQ ID NO:13), PIR Accession Number A29613, Arriza, J.L.; Weinberger, C., Cerelli, G., Glaser, T.M., Handelin, B.L., Housman, D.E., Evans, R.M., Science (1987) 237: 268-275..

Figure 3. GR homology model displayed in ribbon format with dexamethasone (green) and Compound 15 (violet) displayed as space-filling models docked in Site I and Site II, respectively. The location of Site I (dexamethasone site) represents the classical steroid binding site (eg, consistent with the location of progesterone in PR, 1A28). The location of Site II (Compound 15 site) represents the novel binding site which is the subject of this invention.

Figure 4. Twenty-seven analogues used in the correlation of observed AP-1 inhibition and calculated contact energy scores as derived from docking into the homology model of GR Site II. Compound numbers are given to the left of each compound.

Figure 5. The relationship between calculated contact energies of a series of twenty-seven analogues of Compound 15 and their %AP-1 inhibition (at 10μM). Each

analogue was modeled as the S-enantiomer and manually positioned in GR Site II in a manner consistent with the orientation depicted in Figure 3. Energetics were calculated after geometry/energy minimization using Flo (Colin McMartin, Thistlesoft, Colebrook, CT).

Figure 6. Sequence alignments of the GR from various species conducted using the program LOOK (Version 3.5.2, Molecular Applications Group, Palo Alto, CA). The sequence for each GR starts at residue 1. Alignments were made based on pair-wise sequence identity. Site II residues are shaded. Dots are spaceholders and do not represent amino acids. Numbers refer to the first residue in each line, are specific for each GR, and are based on the full-length GR. GR sequences were obtained from the following sources: Squirrel (SEQ ID NO:14) (Saimiri boliviensis boliviensis) (GenBank U87951) Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); Pig GR (SEQ ID NO:15) (GenBank AF141371) Gutscher,M., Eder,S., Mueller,M. and Claus,R. Submitted to GenBank (08-APR-1999) Institut fuer Tierhaltung und Tierzuechtung (470), FG Tierhaltung und Leistungsphysiologie, Universitaet Hohenheim, Garbenstr. 17, Stuttgart 70599, Germany; Guinea Pig (SEQ ID NO:16) (GenBank L13196) Keightley,M.C. and Fuller,P.J. Mol. Endocrinol. 8 (4), 431-439 (1994); Marmoset (SEQ ID NO:17) (GenBank U87953) Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); Ma'z Monkey (SEQ ID NO:18) (GenBank U87952) Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); rat (SEQ ID NO:19) (GenBank M14053) Miesfeld,R., Rusconi,S., Godowski,P.J., Maler,B.A., Okret,S., Wikstrom,A.C., Gustafsson,J.A. and Yamamoto,K.R. Cell 46 (3), 389-399 (1986); mouse (SEQ ID NO:20) (GenBank X04435) Danielsen,M., Northrop,J.P. and Ringold,G.M. EMBO J. 5 (10), 2513-2522 (1986); Human (SEQ ID NO:21) (PIR Accession Number QRHUGA) Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G., Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M., Nature (1985) 318: 635-641.

Figure 7. Ribbon diagram of the LBDs of 11 NHRs detailed in Figure 2, based on a consensus alignment paradigm (ICM, Molsoft LLC, La Jolla, CA). The glucocorticoid receptor (GR) homology model is represented by the blue ribbon.

Figure 8. Graphic demonstration that in a highly sensitive, artificial assay, mutations in Site II inhibit the ability of Site II ligands to induce transactivation, whereas there was a minimal effect on the Site I compound dexamethasone. RLU on the Y-axis is relative light units, a measurement of transactivation. Various mutants and the wild-type are given on the X-axis. Compound A, a Site II ligand, is indicated by the left, darker, solid bar in each pair of bars. Dexamethasone is indicated by the right, lighter, hatched bar in each pair of bars.

Figure 9. Graphic demonstration that the Site I antagonist RU486 inhibits dexamethasone-mediated repression of AP-1 activity, whereas Site II compounds, such as Compound A and Compound B, act in an additive fashion with dexamethasone to repress AP-1 activity. The Y-axis denotes % inhibition of AP-1 activity. The X-axis denotes concentration of dexamethasone. Concentrations of RU486, Compound A, and Compound B are denoted by the indicated symbols.

Figure 10. Graphic demonstration of an assay to indirectly measure the interaction of Site II ligands with GR showing that Site II ligands which do not inhibit dexamethasone on their own can displace other Site II ligands which do inhibit dexamethasone, thereby allowing dexamethasone to bind to GR. Compound D is a Site II ligand that does inhibit dexamethasone. Compound A, Compound B, and Compound C are Site II ligands that do not inhibit dexamethasone on their own. Compound A, Compound B, and Compound C are denoted by the indicated symbols and are the competitor compounds whose concentration is denoted on the X-axis. The Y-axis denotes % inhibition of dexamethasone binding.

Figures 11a and 11b. Graphic demonstrations that a Site II ligand inhibits AP-1-mediated transcription in a GR dependent fashion. The Y-axes denote relative light units (RLU), a measurement of AP-1 activity. On the X-axes, Compound A is a Site

II ligand, DEX is dexamethasone, and PMA is phorbol myristic acid. In Figure 11a, AP-1 activity is measure without the presence of GR. In Figure 11b, AP-1 activity is measured in the presence of GR.

DETAILED DESCRIPTION OF THE INVENTION

We have identified a second binding site in the ligand binding domain of nuclear hormone receptors (NHRs). We refer to this second binding site as Site II.

Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. That is, a Site II is any structure that falls within the given root mean square deviation. Table I is located under the heading for Example 21.

Figure 2 shows the amino acids of Site II in various human NHRs. The structure coordinates of Site II in the NHRs of Figure 2 are given in Table III, located under the heading for Example 22. Two sets of xray structure coordinates of Site II in GR are given in Table IV, located under the heading for Example 23, and Table V, located under the heading for Example 24. Figure 6 shows the amino acids of Site II in the GR of various species.

We have found that ligands of Site II modulate NHRs. Ligands of Site II induce transrepression. Ligands of Site II possess dissociated activity. Ligands of Site II antagonize transactivation.

For all of the present inventions described further below, the following information on possible and preferable embodiments applies.

Said Site II preferably is a nuclear hormone receptor (NHR) Site II, more preferably steroid hormone receptor (SHR) Site II, most preferably a glucocorticoid receptor (GR) Site II.

Said NHR is preferably an SHR, more preferably a GR.

Preferably said NHR is selected from the group consisting of: RXR-alpha; RXR-beta; progesterone receptor (PR); androgen receptor (AR); estrogen receptor-alpha (ER-alpha); ER-beta; vitamin D receptor (VitDR); peroxisome proliferator

activated receptor–gamma (PPAR-gamma); thyroid receptor-alpha (TR-alpha); TR-beta; mineralocorticoid receptor (MR); and glucocorticoid receptor (GR). More preferably, said NHR is selected from the group consisting of: RXR-alpha; RXR-beta; progesterone receptor (PR); androgen receptor (AR); vitamin D receptor (VitDR); peroxisome proliferator activated receptor- gamma (PPAR-gamma); thyroid receptor-alpha (TR-alpha); TR-beta; mineralocorticoid receptor (MR); and glucocorticoid receptor (GR). Most preferably, said NHR is selected from the group consisting of: RXR-alpha; RXR-beta; androgen receptor (AR); vitamin D receptor (VitDR); peroxisome proliferator activated receptor-gamma (PPAR-gamma); thyroid receptor-alpha (TR-alpha); TR-beta; mineralocorticoid receptor (MR); and glucocorticoid receptor (GR).

Preferably said SHR is selected from the group consisting of: PR; AR; ER-alpha; ER-beta; MR; and GR. More preferably, said SHR is selected from the group consisting of: PR; AR; MR; and GR. Most preferably, said SHR is selected from the group consisting of: AR; MR; and GR.

Said RXR-alpha Site II preferably is composed of amino acids L236-P244, A272-A273, Q276-W283, G305-S313, H316-R317, A320-V321, T329, L368-G369, and R372 according to Figure 2. Preferably said structure coordinates of said RXR-alpha Site II define the structure of amino acids L236-P244, A272-A273, Q276-W283, G305-S313, H316-R317, A320-V321, T329, L368-G369, and R372 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. By this it is meant that preferably said structure coordinates define the same shape as the structure of the amino acids according to Table III, or as the structure of the residue backbone atoms according to Table II, but not necessarily that the structure coordinates are identical to those of the amino acids or residue backbone atoms in the table, as the structure coordinates may be of a coordinate system other than Cartesian coordinates. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids L236-P244, A272-A273, Q276-W283, G305-S313, H316-R317, A320-V321, T329, L368-G369, and R372 according to Table III.

Said RAR-gamma Site II preferably is composed of amino acids S194-P202, L233-A234, C237-F244, A266-R274, T277-R278, T280-E282, D290, T328-G329

and S332 according to Figure 2. Preferably said structure coordinates of said RAR-gamma Site II define the structure of amino acids S194-P202, L233-A234, C237-F244, A266-R274, T277-R278, T280-E282, D290, T328-G329 and S332 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids S194-P202, L233-A234, C237-F244, A266-R274, T277-R278, T280-E282, D290, T328-G329 and S332 according to Table III.

Said PR preferably is composed of amino acids M692-V698, L721-G722, Q725-W732, S754-G762, W765-R766, K769-H770, P780, F818-L819 and K822 according to Figure 2. Preferably said structure coordinates of said PR Site II define the structure of amino acids M692-V698, L721-G722, Q725-W732, S754-G762, W765-R766, K769-H770, P780, F818-L819 and K822 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids M692-V698, L721-G722, Q725-W732, S754-G762, W765-R766, K769-H770, P780, F818-L819 and K822 according to Table III.

Said AR Site II preferably is composed of amino acids E678-V684, L708-G709, Q712-W719, S741-A749, W752-R753, T756-N757, P767, F805-L806 and K809 according to Figure 2. Preferably said structure coordinates of said AR Site II define the structure of amino acids E678-V684, L708-G709, Q712-W719, S741-A749, W752-R753, T756-N757, P767, F805-L806 and K809 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids E678-V684, L708-G709, Q712-W719, S741-A749, W752-R753, T756-N757, P767, F805-L806 and K809 according to Table III.

Said ER-alpha Site II preferably is composed of amino acids L320-I326, L348-A349, E352-W359, A381-G389, W392-R393, E396, P405, F444-V445 and K448 according to Figure 2. Preferably said structure coordinates of said ER-alpha Site II define the structure of amino acids L320-I326, L348-A349, E352-W359, A381-G389, W392-R393, E396, P405, F444-V445 and K448 according to Table III, or define the structure of the conserved residue backbone atoms according to Table

III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids L320-I326, L348-A349, E352-W359, A381-G389, W392-R393, E396, P405, F444-V445 and K448 according to Table III.

Said ER-beta Site II preferably is composed of amino acids L273-H279, L297-A298, E301-W308, C330-G338, W341-R342, D345, P354, Y393-L394 and K397 according to Figure 2. Preferably said structure coordinates of said ER-beta Site II define the structure of amino acids L273-H279, L297-A298, E301-W308, C330-G338, W341-R342, D345, P354, Y393-L394 and K397 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids L273-H279, L297-A298, E301-W308, C330-G338, W341-R342, D345, P354, Y393-L394 and K397 according to Table III.

Said VitDR Site II preferably is composed of amino acids L136-D144, L182-V183, S186-F193, S215-R223, E226-S227, T229-D231, G238, H279-V280 and M283 according to Figure 2. Preferably said structure coordinates of said VitDR Site II define the structure of amino acids L136-D144, L182-V183, S186-F193, S215-R223, E226-S227, T229-D231, G238, H279-V280 and M283 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids L136-D144, L182-V183, S186-F193, S215-R223, E226-S227, T229-D231, G238, H279-V280 and M283 according to Table III.

Said PPAR-gamma Site II preferably is composed of amino acids Y219-P227, R288-S289, A292-Y299, G321-M329, S332-L333, N335-K336, E343, L384-A385 and I388 according to Figure 2. Preferably said structure coordinates of said PPAR-gamma Site II define the structure of amino acids Y219-P227, R288-S289, A292-Y299, G321-M329, S332-L333, N335-K336, E343, L384-A385 and I388 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids Y219-P227, R288-S289, A292-Y299, G321-M329, S332-L333, N335-K336, E343, L384-A385 and I388 according to Table III.

Said MR Site II preferably is composed of amino acids E743-I749, L772-A773, Q776-W783, S805-A813, W816-R817, K820-H821, P831, Y869-T870 and K873 according to Figure 2. Preferably said structure coordinates of said MR Site II define the structure of amino acids E743-I749, L772-A773, Q776-W783, S805-A813, W816-R817, K820-H821, P831, Y869-T870 and K873 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids E743-I749, L772-A773, Q776-W783, S805-A813, W816-R817, K820-H821, P831, Y869-T870 and K873 according to Table III.

Said TR-beta Site II preferably is composed of amino acids T226-Q235, I267-I268, A271-F278, C300-R308, V311-R312, D314-E316, G324, V362-A363 and Q366 according to Figure 2. Preferably said structure coordinates of said TR-beta Site II define the structure of amino acids T226-Q235, I267-I268, A271-F278, C300-R308, V311-R312, D314-E316, G324, V362-A363 and Q366 according to Table III, or define the structure of the conserved residue backbone atoms according to Table III. More preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids T226-Q235, I267-I268, A271-F278, C300-R308, V311-R312, D314-E316, G324, V362-A363 and Q366 according to Table III.

Said GR Site II preferably is composed of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Figure 2. Preferably said structure coordinates of said GR Site II define the structure of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I, Table III, Table IV or Table V, or define the structure of the aforementioned amino acids according to the structure coordinates disclosed in Bledsoe, et. al., Cell, online publication by Cell Press, July 1, 2002; DOI: 10.1016/S0092867402008176, or define the structure of the conserved residue backbone atoms according to any of the aforementioned. Preferably, said structure coordinates of said Site II are the structure coordinates of Site II amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I, Table III, Table IV or Table V.

Said GR Site II is preferably selected from the group consisting of: human GR Site II composed of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Figure 6; squirrel GR Site II composed of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 accoring to Figure 6; pig GR Site II composed of amino acids E501-V507, L530, G531, Q534-W541, S563-A571, W574, R575, R578, Q579, P589, Y627, L628 and K631 according to Figure 6; guinea pig GR Site II composed of amino acids E531-V537, L560, G561, Q564-W571, S593-A601, W604, R605, K608, Q609, P619, Y557, L558 and K561 according to Figure 6; marmoset GR Site II composed of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Figure 6; ma'z monkey GR Site II composed of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Figure 6; rat GR Site II E555-V561, L584, G585, Q588-W595, S617-A625, W628, R629, R632, Q633, P643, Y681, L682 and K685 according to Figure 6; and mouse GR Site II E543-V549, L572, G573, Q576-W583, S605-A613, W616, R617, R620, Q621, P631, Y669, L670 and K673 according to Figure 6.

Said nuclear hormone receptor can be of any source, preferably human.

Said glucocorticoid receptor can be of any source, preferably human, rat, mouse, sheep, marmoset, squirrel, pig, guinea pig, or m'az monkey. Most preferably said glucorticoid receptor is human.

Said NHR Site II may be native or mutant. Preferably said NHR Site II is a native NHR Site II. Said SHR Site II maybe native or mutant. Preferably said SHR Site II is a native SHR Site II. Said GR Site II may be native or mutant. Preferably said GR Site II is a native GR Site II.

Said Site II may be found on a protein of any source, including mammalian, fungal, bacterial and plant. Preferably said Site II is found on a mammalian protein, more preferably on a human protein.

Preferably the conserved residue backbone atoms of said Site II have a root mean square deviation of less than 1.9, 1.8, 1.7, 1.6 or 1.5 Å, more preferably of less than 1.4, 1.3, 1.2, 1.1, 1.03, 1.02, or 1.0 Å, yet more preferably of less than 0.93, 0.92,

0.9, 0.8, 0.7, 0.6 0.5, 0.4, 0.3, 0.2, or 0.1 Å, most preferably 1.02, 0.92 or 0.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I.

Preferably the conserved residue backbone atoms of said Site II have a root mean square deviation of less than 2.0, 1.9, 1.8, 1.7, 1.6 or 1.5 Å, more preferably of less than 1.4, 1.3, 1.2, 1.1, 1.03, 1.02, or 1.0 Å, yet more preferably of less than 0.93, 0.92, 0.9, 0.8, 0.7, 0.6 0.5, 0.4, 0.3, 0.2, or 0.1 Å, most preferably 1.02, 0.92 or 0.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table IV.

Preferably the conserved residue backbone atoms of said Site II have a root mean square deviation of less than 2.0, 1.9, 1.8, 1.7, 1.6 or 1.5 Å, more preferably of less than 1.4, 1.3, 1.2, 1.1, 1.03, 1.02, or 1.0 Å, yet more preferably of less than 0.93, 0.92, 0.9, 0.8, 0.7, 0.6 0.5, 0.4, 0.3, 0.2, or 0.1 Å, most preferably 1.02, 0.92 or 0.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table V.

Said structure coordinates may be those determined for a Site II to which a ligand is bound or to which no ligand is bound. Said structure coordinates may be those determined for a Site II of a ligand binding domain in which a Site I ligand is bound to Site I. Said structure coordinates may be those determined for a Site II of an NHR that is in monomer, dimer, or other form.

As is illustrated in Figure 3, the cavity circumscribed by Site II and the cavity circumscribed by Site I (in GR, the dexamethasone binding site) share a common wall section. That is, some amino acids are common to both Site II and Site I. However the cavity circumscribed by Site II is distinct from the cavity circumscribed by Site I, as the two cavities are on opposite sides of the common wall. We manually docked dexamethasone into GR Site I (see Example 10) and determined that the following amino acid residues are in contact distance, i.e. within 2-3 Angstroms, of dexamethasone and thus make up GR Site I: M560, L563, N564, L566, G567, Q570, M601, M604, A605, L608, R611, F623, M639, Q642, M646, L732, Y735, C736,

T739 and E748. The following amino acid residues are common to both GR Site I and Site II: L566, G567, Q570, M601, M604, A605 and R611. The following amino acid residues are unique to GR Site II, i.e. they are not part of GR Site I: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Q615, P625, Y663, L664 and K667. The following amino acid residues are unique to GR Site I, i.e. they are not part of GR Site II: M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748. The amino acids in other NHRs and non-human GR corresponding to the above-recited GR amino acids can be seen in Figures 2 and 6 respectively. We have identified Site II in NHRs as a binding site whose ligands modulate NHRs.

We defined Site II through use of structure coordinates of the ligand binding domain (LBD) of the glucocorticoid receptor (GR), which are provided in Table I. The structure coordinates of the LBD of GR were determined using homology modeling, and later confirmed based on the xray structural elucidation of the GR LBD provided in Apolito, et. al., in WO 03/015692 A2, published February 27, 2003, and Kauppi et. al. in the Journal of Biological Chemistry Online, JBC Papers In Press as DOI:10.1074/JBC.M212711200, April 9, 2003. Thus, some description of homology models and structure coordinates is appropriate here.

Homology models are useful when there is no experimental information available on the three-dimensional structure of the protein of interest. A three dimensional model can be constructed on the basis of the known structure of a homologous protein (Greer *et. al.*, 1991, Lesk, *et. al.*, 1992, Cardozo, *et. al.*, 1995, Sali, *et. al.*, 1995). Those of skill in the art will understand that a homology model is constructed on the basis of first identifying a template, or, protein of known structure which is similar to the protein without known structure. This can be accomplished through pairwise alignment of sequences using such programs as the MODELLER module found in InsightII (Accelrys, Inc., San Diego, CA).

Those of skill in the art will understand that a set of structure coordinates for a protein or part of a protein is a relative set of points that define a shape in three dimensions. For a number of reasons, including those that follow below, the structure coordinates that define two identical or almost identical shapes may vary slightly. If variations are within an acceptable standard error as compared to the

original coordinates, the resulting three-dimensional shape is considered to be equivalent. Thus, for example, a ligand that bound to the structure defined by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I would also be expected to bind to a site having a shape that fell within the acceptable error. Such sites with structures within the acceptable standard error are also within the scope of this invention.

Various computational analyses are therefore necessary to determine whether a molecule or a portion thereof is sufficiently similar to all or parts of the disclosed homology model to be considered equivalent. Such analyses may be carried out in current software applications, such as InsightII (Accelrys Inc., San Diego, CA) Version 2000 as described in the User's Guide, online (www.accelrys.com) or software applications available in the SYBYL software suite (Tripos Inc., St. Louis, MO).

Using the superimposition tool in the program InsightII, for instance, comparisons can be made between different structures and different conformations of the same structure. The procedure used in InsightII to compare structures is divided into four steps: 1) load the structures to be compared; 2) define the atom equivalencies in these structures; 3) perform a fitting operation; and 4) analyze the results. Each structure is identified by a name. One structure is identified as the target (i.e., the fixed structure); the second structure (i.e., moving structure) is identified as the source structure. Since atom equivalency within InsightII is defined by user input, for the purpose of this invention we will define equivalent atoms as protein backbone atoms, also known as residue backbone atoms, (N, Cα, C and O) for all residues between the two structures being compared. We will also consider only rigid fitting operations. When a rigid fitting method is used, the moving structure is translated and rotated to obtain an optimum fit with the target structure. The fitting operation uses an algorithm that computes the optimum translation and rotation to be applied to the moving structure, such that the root mean square difference of the fit over the specified pairs of equivalent atoms is an absolute minimum. This number, given in Angstroms (Å), is reported by InsightII.

Three-dimensional coordinates give the location of the centers of all atoms in a protein molecule and are typically expressed as Cartesian coordinates (eg, distances in three directions, each perpendicular to the other), or polar coordinates (eg, sets of angle/distance pairs from a universal origin), or internal coordinates (eg, sets of angle/distance pairs from one atom center to the next). Thus, it is possible that an entirely different set of coordinates could define an identical or similar shape, depending on which coordinate system is used.

Slight variations in the individual coordinates, as emanate from generation of similar homology models using different alignment templates, and/or using different methods in generating the homology model, will have minor effects on the overall shape.

Variations in coordinates may also be generated because of mathematical manipulations of the structure coordinates. For example, the structure coordinates set forth in Table I could be manipulated by fractionalization of the structure coordinates, integer additions or subtractions to sets of the structure coordinates, inversion of the structure coordinates or any combination of the above.

The structure coordinates of an actual xray structure of a protein would be expected to have some variation from the homology model of that very same protein. For example, the location of sidechains may vary to some extent. As examples, the homology model GR Site II coordinates were compared to the GR Site II x-ray structure coordinates available from the disclosures in WO 03/015692 A2, February 27, 2003 Apolito, et. al. and Kauppi et. al., in the Journal of Biological Chemistry Online, JBC Papers In Press as DOI:10.1074/jbc.M212711200, April 9, 2003, RCSB file: 1nhz.pdb (GR LBD bound to an antagonist, RU 486). When the backbone atoms of the homology model Site II residues, ie, E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I were compared, root mean square deviations (rmsds) of 0.92 and 1.02 Å were obtained between the homology model of Table I Site II residues and the Apolito Site II residues, and between the homology model of Table I Site II residues and the Kauppi Site II residues, respectively. These observations underscore the similarity of the Site II homology model structure to actual crystal structures.

Variations in structure coordinates can be due to mutations, additions, substitutions, and/or deletions of amino acids of a protein being studied.

Variations in structure coordinates can be due to variations in proteins whose shape is being described by the structure coordinates given. For instance, rigid fitting operations conducted (see Example 13) between the GR LBD homology model and several closely-related NHRs known to have similar structure and function (ie, progesterone receptor LBD, androgen receptor LBD, estrogen receptor alpha LBD and estrogen receptor beta LBD as examples) yielded Site II root mean square (rms) deviations in conserved residue backbone atom comparisons of 0.57-0.71 Å. These Site II rms deviations could be greater if other variation factors described above were present in the calculations. GR LBDs from non-human species may also have slight variations in shape from that of human GR LBD defined by the structure coordinates in Table I.

For the purpose of this invention, any structure that has a root mean square deviation of residue backbone atoms (N, Cα, C, O) of less than 2.0 Angstroms (Å) when superimposed on the relevant residue backbone atoms described by structure coordinates listed in Table I is considered to be equivalent. Preferably the root mean square deviation is less than 1.9, 1.8, 1.7, 1.6 or 1.5 Å, more preferably of less than 1.4, 1.3, 1.2, 1.1, 1.03, 1.02, or 1.0 Å, yet more preferably of less than 0.93, 0.92, 0.9, 0.8, 0.7, 0.6 0.5, 0.4, 0.3, 0.2, or 0.1 Å, most preferably 1.02, 0.92 or 0.0 Å.

Within the context of the present invention, "conserved" refers to a portion of a protein backbone which is found in common between two proteins. That is, if portions of two proteins are aligned and compared using the three-dimensional coordinates of their residue backbone atoms for super-positioning, and comparison of the structure coordinates of the residue backbone atoms yields an rms of 2.0 Å or less, then the residue backbone atoms are considered to be conserved between the two proteins.

We made the claimed inventions through a series of experiments described below in the Examples. To help in understanding the invention, that series of experiments is summarized here.

Twenty-seven compounds, which are analogues, were synthesized and shown to inhibit GR binding in GR Site I binding assays and to induce transrepression in

AP-1 cellular transrespressional assays. Some of these compounds were tested in cellular transcriptional assays and shown to induce none to minimal transactivation. Thus these compounds were shown to have dissociated activity.

Twelve analogues of the twenty-seven compounds (some of which are among the twenty-seven compounds) were synthesized and the racemic mixtures were separated into enantiomers. Each of these twenty-four enantiomers was tested in the GR binding assay and the cellular transrepressional assay. It was observed that the S enantiomer of each pair induced AP-1 inhibitory activity when GR was present but did not inhibit well dexamethasone binding to GR, while the R enantiomer of each pair induced minimal AP-1 inhibitory activity when GR was present and inhibited well dexamethasone binding to GR. Each enantiomer was also tested in the cellular transcriptional assay and induced none to minimal transactivation. This suggested that there is an alternate site on GR to which these compounds bind that does not result in inhibition of dexamethasone binding to GR.

A homology model of the ligand binding domain (LBD) of GR was constructed using the known crystal structure of the progesterone receptor (PR). Site II in the LBD of GR was identified by the complementarity of three-dimensional shape and functional features between the Site II and compounds having AP-1 inhibitory activity. Manual docking of one such compound was performed and confirmed the identity of Site II and its role in transrepression. Binding energetics of the S enantomer of the twenty-seven compounds to Site II were calculated and correlated with AP-1 inhibitory activity of these compounds. This positive correlation further confirmed the identity and role of Site II.

As binding energetics to Site II correlates to AP-1 inhibitory activity and all compounds that were tested for binding to Site II are dissociated compounds, Site II was determined to be a target for compounds that have AP-1 inhibitory activity as well as compounds that have dissociated activity.

Additional studies were performed to elucidate the relationship between binding at Site II and binding at Site I. One S enantiomer and dexamethasone were used concurrently in cellular transrepressional assays and cellular transcriptional assays. In the cellular transrepressional assays, it was observed that the dissociated compound (i.e. the S enantiomer) and dexamethasone had an additive effect on AP-

1 inhibitory activity. In the cellular transcriptional assays, it was observed that the presence of a dissociated compound along with dexamethasone reduced transactivation as compared to dexamethasone alone.

The cellular transcriptional assay was performed with a titration of dexamethasone in the presence or absence of each of both enantiomers of a pair. Again, an additive effect on AP-1 inhibitory activity was seen with each of the enantiomers and dexamethasone. In contrast, the Site I antagonist RU 486 inhibited the ability of dexamethasone to induce transrepression.

Other studies performed have shown that mutations in Site II alter the ability of an S enantiomer to modulate GR function. In a highly sensitive, artificial assay system to measure transactivation, it was shown that mutations of residues 543 or 607 prevented the compound from inducing transactivation, whereas, in the wild type protein transactivation was seen. Dexamethasone induced transactivation in both the mutants and the wild type protein.

A further study demonstrated that both an S enantiomer and dexamethasone act in a GR-dependent fashion.

The studies performed to date suggest that both enantiomers interact with Site II. Example 17 shows that both enantiomers R (Compound B) and S (Compound A) act in an additive fashion with saturating levels of dexamethasone to suppress AP-1 activity. Since dexamethasone binds to Site I, it is most likely that the R and S enantiomers interact with Site II to allosterically enhance the repressive activity.

The following definitions are provided to more fully describe the present invention in its various aspects. The definitions are intended to be useful for guidance and elucidation, and are not intended to limit the disclosed invention and its embodiments. Additional definitions may be provided elsewhere in the specification.

The terms "nuclear hormone receptor" and "NHR," as used herein, refer to a member of the nuclear hormone receptor family of transcription factors which bind low molecular weight ligands and stimulate or repress transcription. NHRs include, but are not limited to, glucocorticoid receptors (GRs), progesterone receptors (PRs), androgen receptors (ARs), estrogen receptors (ERs), mineralocorticoid receptors

(MRs), retinoid receptors (RXRs and RARs), Vitamin D receptors (VitDRs), thyroid receptors (TRs), peroxisome proliferator activated receptors (PPARs), and orphan nuclear receptors (i.e. receptors for which the ligands are not yet identified) that bind nuclear hormones. "Nuclear hormone receptor" includes orphan nuclear receptors, which are gene products that embody structural features of nuclear hormone receptors and were identified without any prior knowledge of their association with a putative ligand.

The structural features that define a nuclear hormone receptor, including an orphan nuclear receptor, are the four following features (as disclosed in Giguere , V. (1999) Endocrine Reviews 20(5) p689: 1. An NHR has a modulator domain including the AF-1 domain responsible in part for transcriptional activation function. Modulator domains can also include regions for promoters and cell-specific cofactors and can interact with steroid receptor co-activators (SRCs). 2. An NHR has a DNA binding domain (DBD) composed of two zinc finger modules composed of 60-70 amino acids and a carboxy-terminal extension (CTE) that providesprotein-protein and protein-DNA interactions upon homo- or heterodimer receptorbinding. 3. An NHR has a hinge region that is the hinge between the DBD and the carboxy-terminal ligand binding domain. The hinge region is variable is primary structure and amino acid sequence length. 4. An NHR has a ligand binding domain (LBD) that contains the AF-2 motif (which corresponds to helix 12 of NHRs) and provides a structured region whereby AF-2 (helix 12) is packed closely to the LBD core forming an interface with at least 3 other helices of the core. The interface is involved with binding of co-activator or co-repressor polypeptides.

"Nuclear hormone receptor" and "NHR," as used herein, refer to NHRs from any source, including but not limited to: glucocorticoid receptor as disclosed in Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G., Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M., Nature (1985) 318: 635-641 ; progesterone receptor as disclosed in Misrahi, M. et al. (1987) Biochem. Biophys. Res. Commun. 143, p740; androgen receptor as disclosed in Lubahn D. B., et al (1988); estrogen receptors as disclosed in Green, S., et al. (1986) Nature 320, p134); mineralocorticoid receptor as disclosed in Arriza, J.L., et al., (1987) Science 237,

p268; retinoid receptors (RXRs and RARs) as disclosed in Mangelsdorf, et al. (1990) Nature, 345, p224 and Petkovich M., et al (1987) Nature 330, p444; Vitamin D receptor, thyroid receptor (TR) as disclosed in Nakai, A. et al., (1988) Mol. Endocrinol. 2, p1087; peroxisome proliferator activated receptor (PPAR) as disclosed in Greene, M.E., et al. (1995) Gene Expression 4, p281; RXRalpha (1lbd) as disclosed in Bourguet, W., Ruff, M., Chambon, P., Gronemeyer, H., Moras, D. Nature 375 pp. 377 (1995); PPARgamma (2prg) as disclosed in Nolte, R. T., Wisely, G. B., Westin, S., Cobb, J. E., Lambert, M. H., Kurokawa, R., Rosenfeld, M. G., Willson, T. M., Glass, C. K., Milburn, M. V. Nature 395 pp. 137 (1998); RARgamma (2lbd) as disclosed in Renaud, J. P., Rochel, N., Ruff, M., Vivat, V., Chambon, P., Gronemeyer, H., Moras, D. Nature 378 pp. 681 (1995); PR (1a28) as disclosed in Williams, S. P., Sigler, P. B. Nature 393 pp. 392 (1998); VitDR (1db1) as disclosed in Rochel, N., Wurtz, J. M., Mitschler, A., Klaholz, B., Moras, D. Mol. Cell 5 pp. 173 (2000); AR (1e3g) as disclosed in Matias, P. M., Donner, P., Coelho, R., Thomaz, M., Peixoto, C., Macedo, S., Otto, N., Joschko, S., Scholz, P., Wegg, A., Basler, S., Schafer, M., Egner, U., Carrondo, M. A. J.Biol.Chem. 275 pp. 26164 (2000); ERalpha (1a52) as disclosed in Tanenbaum, D. M., Wang, Y., Williams, S. P., Sigler, P. B. Proc Natl Acad Sci U S A 95 pp. 5998 (1998); ERbeta (1l2j) as disclosed in Shiau, A. K., Barstad, D., Radek, J. T., Meyers, M. J., Nettles, K. W., Katzenellenbogen, B. S., Katzenellenbogen, J. A., Agard, D. A., Greene, G. L. Nat.Struct.Biol. 9 pp. 359 (2002); TRbeta (1bsx) as disclosed in Wagner, R. L., Darimont, B. D., Apriletti, J. W., Stallcup, M. R., Kushner, P. J., Baxter, J. D., Fletterick, R. J., Yamamoto, K. R. Genes Dev. 12 pp. 3343 (1998); GR, PIR Accession Number QRHUGA, as dislcosed in Hollenberg, S.M., Weinberger, C., Ong, E.S.; Cerelli, G., Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M., Nature (1985) 318: 635-641; MR, PIR Accession Number A29613, as disclosed in Arriza, J.L.; Weinberger, C., Cerelli, G., Glaser, T.M., Handelin, B.L., Housman, D.E., Evans, R.M., Science (1987) 237: 268-275. Orphan nuclear receptors include but are not limited to: Rev Erb(alpha) (1hlz) as disclosed in Sierk, M.L., et. al., Biochemistry (2001) 40: pp. 12833; Pxr (1ilh) as disclosed in Watkins, R.E., et. al., Science (2002) 292: pp. 2329; ERR3 (1kv6) as disclosed in Greschik, H., et. al., Mol. Cell (2002) 9: pp. 303; Nurrl (1ovl) as disclosed in Wang, Z., et. al., Nature (2003) 423: pp. 555; ERR1 as disclosed in

Guiguere, V., et al., Nature (1988) 331: 91-94. Other NHRs, including orphan nuclear receptors, include those disclosed in: The Nuclear Receptor Facts Book, V. Laudet and H. Gronemeyer, Academic Press, p345, 2002; and Francis et al, Annu. Rev. Physiol. 2003, 65:261-311.

The terms "steroid hormone receptor" and "SHR," as used herein, refer to a member of the nuclear hormone receptor family of transcription factors which bind steroids and stimulate or repress transcription. SHRs include, but are not limited to, glucocorticoid receptors (GRs), progesterone receptors (PRs), androgen receptors (ARs), estrogen receptors (ERs), mineralocorticoid receptors (MRs), and orphan receptors (i.e. receptors for which the ligands are not yet identified) that bind steroids. These terms, as used herein, refer to steroid hormone receptors from any source, including but not limited to human.

The terms "glucocorticoid receptor" and "GR," as used herein, refer to a member of the nuclear hormone receptor family of transcription factors which bind glucocorticoids and stimulate or repress transcription, and to the GR-beta isoform. These terms, as used herein, refer to glucocorticoid receptor from any source, including but not limited to: human glucocorticoid receptor as disclosed in Weinberger, et al. Science 228, p740-742, 1985, and in Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G., Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M.; Nature (1985) 318: 635-641,; rat glucocorticoid receptor as disclosed in Miesfeld, R. Nature, 312, p779-781, 1985; mouse glucocortoid receptor as disclosed in Danielson, M. et al. EMBO J., 5, 2513; sheep glucocorticoid receptor as disclosed inYang, K., et al. J. Mol. Endocrinol. 8, p173-180, 1992; marmoset glucocortoid receptor as disclosed in Brandon, D.D., et al, J. Mol. Endocrinol. 7, p89-96, 1991; human GR-beta as disclosed in Hollenberg, SM. et al. Nature, 318, p635, 1985, Bamberger, C.M. et al. J. Clin Invest. 95, p2435, 1995; Squirrel (Saimiri boliviensis boliviensis) (GenBank U87951) as disclosed in Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); Pig GR (GenBank AF141371) as disclosed in Gutscher,M., Eder,S., Mueller,M. and Claus,R. Submitted to GenBank (08-APR-1999) Institut fuer Tierhaltung und Tierzuechtung (470), FG Tierhaltung und Leistungsphysiologie, Universitaet Hohenheim, Garbenstr. 17, Stuttgart 70599, Germany; Guinea Pig (GenBank L13196) as disclosed in

Keightley,M.C. and Fuller,P.J. Mol. Endocrinol. 8 (4), 431-439 (1994); Marmoset (GenBank U87953) as disclosed in Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); Ma'z Monkey (GenBank U87952) as disclosed in Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); rat (GenBank M14053) as disclosed in Miesfeld,R., Rusconi,S., Godowski,P.J., Maler,B.A., Okret,S., Wikstrom,A.C., Gustafsson,J.A. and Yamamoto,K.R. Cell 46 (3), 389-399 (1986); mouse (GenBank X04435) as disclosed in Danielsen,M., Northrop,J.P. and Ringold,G.M. EMBO J. 5 (10), 2513-2522 (1986); Human (Protein Information Resource (PIR) Accession Number QRHUGA) as disclosed in Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G., Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M., Nature (1985) 318: 635-641.

The term "binding site," as used herein, refers to a region of a molecule or molecular complex that, as a result of its shape, favorably associates with, i.e. binds, another molecule, such other molecule being a ligand of the binding site. A binding site, such as Site II, is analogous to a wall and circumscribes a space referred to as a "cavity" or "pocket." The ligand of the binding site situates in the cavity.

The terms "binds" in all its grammatical forms, as used herein, refers to a condition of proximity between or amongst molecules, chemical compounds or chemical entities. The association may be non-covalent (i.e. non-bonded or reversible), wherein the juxtaposition is energetically favored by hydrogen bonding or van der Waals or electrostatic interactions, or it may be covalent (i.e. bonded or irreversible).

The term "soaked," as used herein, refers to a process in which the protein crystal is transferred to a solution containing the compound of interest.

The terms "at least a portion of," "a portion of," "any part of," and "any portion of," in all their grammatical forms, as used herein when referring to Site II, or the structure coordinates of Site II, or the cavity circumscribed by Site II, refer to all or any part of Site II, or the structure coordinates of Site II, or the cavity circumscribed by Site II, wherein Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the

structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. Preferably the terms relate to a sufficient number of residues or the corresponding structure coordinates so as to be useful in docking or modeling a ligand in the cavity circumscribed by Site II. Preferably, the terms comprise one or more of the following residues or the corresponding structure coordinates: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Q615, P625, Y663, L664 and K667. These are the residues of Site II that are not also part of Site I. More preferably, the terms comprise one or more of the following residues or the corresponding structure coordinates: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Y663, L664 and K667. Preferably, the terms relate to at least four amino acid residues, more preferably at least five amino acids, more preferably at least eight amino acid residues, more preferably at least fifteen amino acid residues, more preferably at least twenty amino acid residues, more preferably at least twenty-five amino acid residues, most preferably at least thirty amino acid residues.

The term "mutant," as used herein, refers to a protein, or portion of protein, having one or more amino acid deletions, insertions, inversions, repeats, or substitutions as compared to the relevant native protein or relevant portion of native protein. A native protein is one occurring in nature. A mutant Site II falls within the scope of this invention so long as the rms deviation in conserved residue backbone atoms between such mutant Site II and the the Site II residues according to Table I falls within 2.0 Angstroms. A mutant may have the same, similar, or altered activity as compared to the native protein. Activity refers to transrepression, transactivation, and ligand binding. Preferred mutants have at least 25% sequence identity, more preferably at least 50% sequence identity, more preferably at least 75% sequence identity, and most preferably at least 95% sequence identity to the native protein or portion of native protein.

The term "root mean square deviation" means the square root of the arithmetic mean of the squares of the deviations from the mean. It is a way to express the deviation or variation from a trend or object. For purposes of this invention, the "root mean square deviation" defines the variation in the backbone of a protein or portion of

a protein from the relevant portion of the backbone of another protein, such as the LBD defined by the structure coordinates of Table I.

The term "structure coordinates," "structural coordinates," "atomic coordinates," or "atomic structure coordinates" refers to coordinates that specify the location of the centers of atoms in a protein molecule or molecular complex. The terms include, but are not limited to, Cartesian coordinates, polar coordinates, and internal coordinates. The structure coordinates may be generated by any means, including the building of a homology model or derivation from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of a molecule or molecular complex in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are then used to establish the positions of the individual atoms of the molecule or molecular complex.

The term "molecule," as used herein, has the meaning generally used in the art and includes, but is not limited to, proteins, nucleic acids, and chemical compounds, including small organic compounds. "Small organic compounds" are also known as "small organic molecules" or "small molecules."

The term "complex" or "molecular complex," as used herein, refers to a covalent or non-covalent association of a molecule with its ligand.

The term "chemical entity," as used herein, refers to chemical compounds, complexes of at least two chemical compounds, and fragments of such chemical compounds or complexes. A modulator may be a chemical entity. A ligand may be a chemical entity.

The term "compound," as used herein, refers to a chemical compound.

The term "test molecule," as used herein, refers to a molecule, preferably a chemical compound, that is being tested for specific characteristics.

The term "ligand," as used herein, refers to a molecule that binds to another molecule or portion of another molecule.

The term "modulator," as used herein, refers to a molecule whose presence induces an activity in the molecule that it modulates. A modulator can bind to the molecule that it modulates, i.e. be a ligand of the molecule it modulates. A preferred modulator is a ligand of the molecule that it modulates. Modulators include, but are

not limited to, small organic molecules, chemical compounds, peptides, peptidomimetics (eg., cyclic peptides, peptide analogs, or constrained peptides) and nucleic acids. Modulators can be natural or synthetic. Preferred modulators are small organic molecules.

The term "modeling" in all its grammatical forms, as used herein, refers to the development of a mathematical construct designed to mimic real molecular geometry and behavior in proteins and small molecules. These mathematical constructs include, but are not limited to: energy calculations for a given geometry of a molecule utilizing forcefields or ab initio methods known in the art; energy minimization using gradients of the energy calculated as atoms are shifted so as to produce a lower energy; conformational searching, ie, locating local energy minima; molecular dynamics wherein a molecular system (single molecule or ligand/protein complex) is propagated forward through increments of time according to Newtonian mechanics using techniques known to the art; calculations of molecular properties such as electrostatic fields, hydrophobicity and lipophilicity; calculation of solvent-accessible or other molecular surfaces and rendition of the molecular properties on those surfaces; comparison of molecules using either atom-atom correspondences or other criteria such as surfaces and properties; quantitiative structure-activity relationships in which molecular features or properties dependent upon them are correlated with activity or bio-assay data.

The term "fits spatially" in all its grammatical forms, as used herein, refers to when the three-dimensional structure of a compound is accommodated geometrically by a cavity or pocket of a protein, such as the cavity circumscribed by Site II.

The terms "docking" and "performing a fitting operation," in all their grammatical forms, as used herein, refer to the computational placement of a chemical entity (eg. a potential ligand, preferably a small organic molecule) within a space (i.e. cavity) at least partially enclosed by the protein structure (i.e. binding site) so that structural and chemical feature complementarity (i.e. binding contacts) between chemical entity and binding site components can be assessed in terms of interactions typical of protein/ligand complexes. Specifically, the structural and chemical features may include both bonded and non-bonded interactions, and more generally, the non-bonded interactions which occur in the bulk of reversible protein/ligand complexes

would include forces such as hydrogen-bonding, electrostatic or charge interactions, vander Waal's interactions, and hydrophobic interactions. Such placement could be conducted manually or automatically using software designed for such purpose.

The term "transrepress" or "transrepression," in all their grammatical forms, is used herein to refer to the process in which an NHR represses transcription by inhibiting a transcription factor or coactivator from inducing transcription. The term is not limited to any specific mechanism of action, any specific transcription factor or coactivator, or any specific gene whose transcription is repressed. AP-1 and NF-κB are two transcription factors, among others, that can be inhibited by an NHR.

The term "transactivate" or "transactivation," in all their grammatical forms, is used herein to refer to the process in which an NHR stimulates transcription, either by binding to DNA and inducing transcription, or by modulating the activity of another DNA binding protein that induces transcription. The term is not limited to any specific mechanism of action or any specific gene whose transcription is stimulated.

The term, "NF-κB-dependent gene expression," as used herein, refers to the expression of those genes that are under the regulatory control of the NF-κB transcription factor. Such genes include, but are not limited to the immune-related and inflammatory genes encoding TNF-alpha, IL-1, IL-2, IL-5, adhesion molecules (such as E-selectin), chemokines (such Eoxtaxin and Rantes), and Cox-2.

The term, "AP-1-dependent gene expression," as used herein, refers to the expression of genes that are under the regulatory control of the AP-1 transcription factor. Such genes include, but are not limited to the immune-related and inflammatory genes encoding TNF-alpha, IL-1, IL-2, IL-5, adhesion molecules (such as E-selectin), chemokines (such Eoxtaxin and Rantes), and Cox-2.

The term "dissociated compound" is used herein to refer to a modulator of an NHR that induces transrepression and induces none to minimal transactivation. The term "dissociated activity" refers to the activity in which a dissociated compound induces transrepression and induces none to minimal transactivation.

The term "treat", "treating", or "treatment," in all grammatical forms, as used herein refers to the prevention, reduction, or amelioration, partial or complete alleviation, or cure of a disease, disorder, or condition.

The term "NHR-associated disease," as used herein, refers to a disease or disorder associated with the expression product of a gene whose transcription is stimulated or repressed by an NHR. Stimulation is through transactivation. Repression is through transrepression. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders, diseases associated with AP-1-dependent gene expression, diseases associated with NF-κB-dependent gene expression, diseases associated with NHR transrepression, diseases associated with NHR transactivation, diseases treatable by inducing NHR transrepression, and diseases treatable by antagonizing NHR transactivation.

The term "SHR-associated disease," as used herein, refers to a disease or disorder associated with the expression product of a gene whose transcription is stimulated or repressed by an SHR. Stimulation is through transactivation. Repression is through transrepression. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders, diseases associated with AP-1-dependent gene expression, diseases associated with NF-κB-dependent gene expression, diseases associated with SHR transrepression, diseases associated with SHR transactivation, diseases treatable by inducing SHR transrepression, and diseases treatable by antagonizing SHR transactivation.

The term "GR-associated disease," as used herein, refers to a disease or disorder associated with the expression product of a gene whose transcription is stimulated or repressed by a GR. Stimulation is through transactivation. Repression is through transrepression. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders, diseases associated with AP-1-dependent gene expression, diseases associated with NF-κB-dependent gene expression, diseases associated with NHR transrepression, diseases associated with GR transactivation, diseases treatable by inducing GR transrepression, and diseases treatable by antagonizing GR transactivation.

The term "disease associated with NHR transrepression," as used herein, refers to a disease or disorder associated with the transcription product of a gene whose transcription is transrepressed by an NHR. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders, diseases associated with NF-κB-dependent gene expression, diseases, diseases associated with

AP-1-dependent gene expression, and diseases treatable by inducing NHR transrepression.

The term "disease associated with SHR transrepression," as used herein, refers to a disease or disorder associated with the transcription product of a gene whose transcription is transrepressed by an SHR. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders, diseases associated with NF-κB-dependent gene expression, diseases, diseases associated with AP-1-dependent gene expression, and diseases treatable by inducing SHR transrepression.

The term "disease associated with GR transrepression," as used herein, refers to a disease or disorder associated with the transcription product of a gene whose transcription is transrepressed by a GR. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders, diseases associated with NF-κB-dependent gene expression, diseases, diseases associated with AP-1-dependent gene expression, and diseases treatable by inducing GR transrepression.

The term "disease associated with NHR transactivation," as used herein, refers to a disease or disorder associated with the transcription product of a gene whose transcription is transactivated by an NHR. Such diseases include, but are not limited to: osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes, hypertension, obesity, depression, AIDS, the condition of wound healing, prostate cancer, breast cancer, primary or secondary andrenocortical insufficiency, and Addison's disease.

The term "disease associated with SHR transactivation," as used herein, refers to a disease or disorder associated with the transcription product of a gene whose transcription is transactivated by an SHR. Such diseases include, but are not limited to: osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes, hypertension, obesity, depression, and AIDS, the condition of wound healing, prostate cancer, breast cancer, primary or secondary andrenocortical insufficiency, and Addison's disease.

The term "disease associated with GR transactivation," as used herein, refers to a disease or disorder associated with the transcription product of a gene whose transcription is transactivated by a GR. Such diseases include, but are not limited to: osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes,

hypertension, obesity, depression, and AIDS, the condition of wound healing, primary or secondary andrenocortical insufficiency, and Addison's disease.

The term, "disease associated with NF-κB-dependent gene expression," as used herein, refers to a disease or disorder associated with the expression product of a gene under the regulatory control of NF-κB. Such diseases include, but are not limited to: inflammatory and immune associated diseases and disorders; cancer and tumor disorders, such as solid tumors, lymphomas and leukemia; fungal infections such as mycosis fungoides; ischemic or reperfusion injury such as ischemic or reperfusion injury that may have been incurred during organ transplantation, myocardial infarction, stroke or other causes; and DNA and RNA viral replication diseases, such herpes simplex type 1 (HSV-1), herpes simplex type 2 (HSV-2), hepatitis (including hepatitis B and hepatitis C), cytomegalovirus, Epstein-Barr, and human immunodeficiency virus (HIV).

The term, "disease associated with AP-1-dependent gene expression," as used herein, refers to a disease or disorder associated with the expression product of a gene under the regulatory control of AP-1. Such diseases include, but are not limited to: inflammatory and immune associated diseases and disorders; cancer and tumor disorders, such as solid tumors, lymphomas and leukemia; and fungal infections such as mycosis fungoides.

The term "inflammatory or immune associated diseases or disorders" is used herein to encompass any condition, disease, or disorder that has an inflammatory or immune component, including,but not limited to, each of the following conditions: transplant rejection (e.g., kidney, liver, heart, lung, pancreas (e.g., islet cells), bone marrow, cornea, small bowel, skin allografts, skin homografts (such as employed in burn treatment), heart valve xenografts, serum sickness, and graft vs. host disease, autoimmune diseases, such as rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, juvenile diabetes, asthma, inflammatory bowel disease (such as Crohn's disease and ulcerative colitus), pyoderma gangrenum, lupus (systemic lupus erythematosis), myasthenia gravis, psoriasis, dermatitis, dermatomyositis; eczema, seborrhoea, pulmonary inflammation, eye uveitis, hepatitis, Grave's disease, Hashimoto's thyroiditis, autoimmune thyroiditis, Behcet's or Sjorgen's syndrome (dry eyes/mouth), pernicious or immunohaemolytic anaemia, atherosclerosis, Addison's

disease (autoimmune disease of the adrenal glands), idiopathic adrenal insufficiency, autoimmune polyglandular disease (also known as autoimmune polyglandular syndrome), glomerulonephritis, scleroderma, morphea, lichen planus, viteligo (depigmentation of the skin), alopecia areata, autoimmune alopecia, autoimmune hypopituatarism, Guillain-Barre syndrome, and alveolitis; T-cell mediated hypersensitivity diseases, including contact hypersensitivity, delayed-type hypersensitivity, contact dermatitis (including that due to poison ivy), uticaria, skin allergies, respiratory allergies (hayfever, allergic rhinitis) and gluten-sensitive enteropathy (Celiac disease); inflammatory diseases such as osteoarthritis, acute pancreatitis, chronic pancreatitis, asthma, acute respiratory distress syndrome, Sezary's syndrome and vascular diseases which have an inflammatory and or a proliferatory component such as restenosis, stenosis and artherosclerosis. Inflammatory or immune associated diseases or disorders also includes, but is not limited to: endocrine disorders, rheumatic disorders, collagen diseases, dermatologic disease, allergic disease, opthalmic disease, respiratory disease, hematologic disease, gastrointestinal disease, inflammatory disease, autoimmune disease, Congenital adrenal hyperplasia, Nonsuppurative thyroiditis, Hypercalcemia associated with cancer, Psoriatic arthritis, Rheumatoid arthritis, including juvenile rheumatoid arthritis, Ankylosing spondylitis, Acute and subacute bursitis, Acute nonspecific tenosynovitis, Acute gouty arthritis, Post-traumatic osteoarthritis, Synovitis of osteoarthritis, Epicondylitis, Systemic lupus erythematosus, Acute rheumatic carditis,Pemphigus, Bullous dermatitis herpetiformis, Severe erythema multiforme, Exfoliative dermatitis, Psoriasis, Seborrheic dermatitis, Seasonal or perennial allergic rhinitis, Serum sickness, Bronchial asthma, Contact dermatitis, Atopic dermatitis, Drug hypersensitivity reactions, Allergic conjunctivitis, Keratitis, Herpes zoster ophthalmicus, Iritis and iridocyclitis, Chorioretinitis, Optic neuritis, Symptomatic sarcoidosis, Fulminating or disseminated pulmonary tuberculosis chemotherapy, Idiopathic thrombocytopenic purpura in adults, Secondary thrombocytopenia in adults, Acquired (autoimmune) hemolytic anemia, Leukemias and lymphomas in adults, Acute leukemia of childhood, Ulcerative colitis, Regional enteritis, Crohn's diease, Sjogren's syndrome, Autoimmune vasculitis, Multiple sclerosis, Myasthenia

gravis, Anklyosing spondylitis, Chronic obstructive pulmonary disease, Solid organ transplant rejection, Sepsis, and Allergy.

The term "disease treatable by inducing NHR transrepression," as used herein, refers to a disease that can be treated by inducing NHR transrepression. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders.

The term "disease treatable by inducing SHR transrepression," as used herein, refers to a disease that can be treated by inducing SHR transrepression. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders.

The term "disease treatable by inducing GR transrepression," as used herein, refers to a disease that can be treated by inducing GR transrepression. Such diseases include, but are not limited to, inflammatory and immune associated diseases and disorders.

The term "disease treatable by antagonizing NHR transactivation," as used herein, refers to a disease that can be treated by antagonizing NHR transactivation. Such diseases include, but are not limited to: osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes, hypertension, obesity, depression, and AIDS, the condition of wound healing, prostate cancer, breast cancer, and primary or secondary andrenocortical insufficiency.

The term "disease treatable by antagonizing SHR transactivation," as used herein, refers to a disease that can be treated by antagonizing SHR transactivation. Such diseases include, but are not limited to: osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes, hypertension, obesity, depression, and AIDS, the condition of wound healing, prostate cancer, breast cancer, and primary or secondary andrenocortical insufficiency.

The term "disease treatable by antagonizing GR transactivation," as used herein, refers to a disease that can be treated by antagonizing GR transactivation. Such diseases include, but are not limited to: osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes, hypertension, obesity, depression, and AIDS, the condition of wound healing, prostate cancer, breast cancer, and primary or secondary andrenocortical insufficiency.

Machine –Readable Data Storage Media, and Computer Systems

We have identified a second binding site in the ligand binding domain of NHRs, termed Site II, and provide herein the structure coordinates of Site II. The structure coordinates may be used in the design and identification of ligands of Site II and modulators of NHRs. In order to so-use structure coordinates, it may be necessary to convert them into a three-dimensional shape. This is achieved through the use of commercially available software that, in conjunction with a computer, is capable of generating three-dimensional graphical representations of molecules or portions thereof from a set of structure coordinates provided on a machine-readable data storage medium.

Therefore, the invention provides a machine-readable data storage medium comprising a data storage material encoded with machine-readable data comprising all or any part of structure coordinates of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I.

The invention also provides a machine-readable data storage medium comprising a data storage material encoded with machine readable data consisting of all or any part of structure coordinates of a Site II.

As is illustrated in Figure 3, the cavity circumscribed by Site II and the cavity circumscribed by Site I share a common wall section. That is, some amino acids are common to both Site II and Site I. However the cavity circumscribed by Site II is distinct from the cavity circumscribed by Site I, as the two cavities are on opposite sides of the common wall. We manually docked dexamethasone into GR Site I (see Example 10) and determined that the following amino acid residues are in contact distance, i.e. within 2-3 Angstroms, of dexamethasone and thus make up GR Site I: M560, L563, N564, L566, G567, Q570, M601, M604, A605, L608, R611, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748. The following amino acid residues are common to both GR Site I and Site II: L566, G567, Q570, M601, M604,

A605 and R611. The following amino acid residues are unique to GR Site II, i.e. they are not part of GR Site I: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Q615, P625, Y663, L664 and K667. The following amino acid residues are unique to GR Site I, i.e. they are not part of GR Site II: M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748. The amino acids in other NHRs and non-human GR corresponding to the above-recited GR amino acids can be seen in Figures 2 and 6 respectively. Site II and its function were newly identified by us, who were the first to identify Site II in NHRs as a binding site whose ligands modulate NHRs.

Thus the invention also provides a machine-readable data storage medium comprising a data storage material encoded with machine readable data, wherein the data: (a) comprises all or any part of the structure coordinates of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; and (b) does not comprise structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of one or more of amino acids M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748 according to Table I. Preferably, said data does not comprise structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of all of amino acids M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748 according to Table I. Preferably, the root mean square deviation of part (b) is less than 1.9, 1.8, 1.7, 1.6 or 1.5 Å, more preferably of less than 1.4, 1.3, 1.2, 1.1, 1.03, 1.02, or 1.0 Å, yet more preferably of less than 0.93, 0,92, 0.9, 0.8, 0.7, 0.6 0.5, 0.4, 0.3, 0.2, or 0.1 Å, most preferably 1.02, 0.92 or 0.0 Å.

The machine-readable data storage media of the present invention are used in a computer. The computer is capable of producing a three-dimensional representation

of Site II, and comprises various components, including the machine-readable storage medium, used to produce the three-dimensional representation.

Thus, the invention further provides a computer system capable of producing a three-dimensional representation of all or any part of a Site II, wherein said computer system comprises: (a) a machine-readable data storage medium comprising a data storage material encoded with machine readable data comprising all or any part of structure coordinates of Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; (b) a working memory for storing instructions for processing said machine-readable data; (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine readable data into said three-dimensional representation; and (d) a display coupled to said central-processing unit for displaying said three-dimensional representation.

The invention also provides a computer system as described above wherein the machine-readable data consists of all or any part of the structure coordinates of Site II.

The invention also provides a computer system capable of producing a three-dimensional representation of all or any part of Site II, wherein said computer system comprises: (a) a machine-readable data storage medium comprising a data storage material encoded with machine readable data, wherein the data: (i) comprises all or any part of the structure coordinates of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; and (ii) does not comprise structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms

described by the structure coordinates of one or more of amino acids M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748 according to Table I; (b) a working memory for storing instructions for processing said machine-readable data; (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine readable data into said three-dimensional representation; and (d) a display coupled to said central-processing unit for displaying said three-dimensional representation. Preferably, said data does not comprise structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of all of amino acids M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748 according to Table I.

For all of the present invention, preferably said structure coordinates are Cartesian coordinates, polar coordinates, or internal coordinates. Most preferably said structure coordinates are Cartesian coordinates.

For all of the present invention, preferably said structure coordinates are of at least four amino acids, more preferably of at least five amino acids, more preferably of at least eight amino acids, more preferably of at least fifteen amino acids, more preferably of at least twenty amino acids, more preferably at least twenty-five amino acids, most preferably at least thirty amino acids.

For all of the present invention, said structure coordinates may be those determined for a Site II to which a ligand is bound or to which no ligand is bound. Said structure coordinates may be those determined for a Site II of an NHR that is in monomer, dimer, or other form.

One of ordinary skill in the art will recognize that there can be various embodiments of the components of the computer system. One embodiment of a computer system utilizes System 10 as disclosed in WO 98/11134, the disclosure of which is incorporated herein by reference in its entirety. Briefly, one version of the computer system comprises a central processing unit ("CPU"), a working memory which may be, e.g, RAM (random-access memory) or "core" memory, mass storage memory (such as one or more disk drives or CD-ROM drives), one or more cathode-ray tube ("CRT") display terminals, one or more keyboards, one or more input lines,

and one or more output lines, all of which are interconnected by a conventional bidirectional system bus.

Input hardware, coupled to the computer by input lines, may be implemented in a variety of ways. Machine-readable data of this invention may be inputted via the use of a modem or modems connected by a telephone line or dedicated data line. Alternatively or additionally, the input hardware may comprise CD-ROM drives or disk drives. In conjunction with a display terminal, keyboard may also be used as an input device.

Output hardware, coupled to the computer by output lines, may similarly be implemented by conventional devices. By way of example, output hardware may include a CRT display terminal for displaying a graphical representation of a region or domain of the present invention using a program such as QUANTA as described herein. Output hardware might also include a printer, so that hard copy output may be produced, or a disk drive, to store system output for later use.

In operation, the CPU coordinates the use of the various input and output devices, coordinates data accesses from mass storage, and accesses to and from the working memory, and determines the sequence of data processing steps. A number of programs may be used to process the machine-readable data of this invention. Such programs are discussed in reference to the computational methods of drug discovery as described herein. Specific references to components of the hardware system are included as appropriate throughout the following description of the data storage medium.

For the purpose of the present invention, any magnetic data storage medium which can be encoded with machine-readable data would be sufficient for carrying out the storage requirements of the system. The medium could be a conventional floppy diskette or hard disk, having a suitable substrate, which may be conventional, and a suitable coating, which may be conventional, on one or both sides, containing magnetic domains whose polarity or orientation could be altered magnetically, for example. The medium may also have an opening for receiving the spindle of a disk drive or other data storage device.

The magnetic domains of the coating of a medium may be polarized or oriented so as to encode in a manner which may be conventional, machine readable

data such as that described herein, for execution by a system such as the system described herein.

Another example of a suitable storage medium which could also be encoded with such machine-readable data, or set of instructions, which could be carried out by a system such as the system described herein, could be an optically-readable data storage medium. The medium could be a conventional compact disk read only memory (CD-ROM) or a rewritable medium such as a magneto-optical disk which is optically readable and magneto-optically writable. The medium preferably has a suitable substrate, which may be conventional, and a suitable coating , which may be conventional, usually of one side of substrate.

In the case of a CD-ROM, as is well known, the coating is reflective and is impressed with a plurality of pits to encode the machine-readable data. The arrangement of pits is read by reflecting laser light off the surface of the coating. A protective coating, which preferably is substantially transparent, is provided on top of the reflective coating.

In the case of a magneto-optical disk, as is well known, the coating has no pits, but has a plurality of magnetic domains whose polarity or orientation can be changed magnetically when heated above a certain temperature, as by a laser. The orientation of the domains can be read by measuring the polarization of laser light reflected from the coating. The arrangement of the domains encodes the data as described above.

Methods of Designing and Identifying Ligands of Site II and Modulators of NHRs

The present invention permits the use of structure-based or rational drug design and virtual screening to design or identify potential ligands and modulators of Site II.

The identity of Site II as disclosed herein permits the practice of the following techniques commonly practiced in structure-based design and virtual screening.

Using a three-dimensional model of all or any part of Site II, a test molecule, i.e. potential ligand or potential modulator, can be docked into the cavity circumscribed by Site II, i.e. a fitting operation can be performed between a test molecule and Site II. After docking, the test molecule may be analyzed for structural and chemical feature complementarity with all or any part of Site II. Structural and

chemical features include, but are not limited to, any one of the following: van der Waals interactions, hydrogen bonding interactions, charge interaction, hydrophobic interactions, and dipole interactions.

Therefore, the invention provides a method of docking a test molecule comprising docking the test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. The method may further comprise analyzing structural and chemical feature complementarity of the test molecule with all or any part of said Site II.

A three-dimensional model can be created using methods known in the art, including, but not limited to, using software such as InsightII (Accelrys, Inc., San Diego, CA), SYBYL (Tripos Associates, St. Louis, MO), and Flo (Colin McMartin, Thistlesoft, Colebrook, CT). Docking can be performed manually or using a variety of software, including but not limited to, DOCK (Kuntz *et. al.* 1982), GOLD (Cambridge Crystallographic Data Center, 12 Union Road, Cambridge, UK), or Flo (Thistlesoft, High Meadow, 603 Colebrook Raod, Colebrook, CT). Analyzing structural and chemical feature complementarity includes any process of a) quantifying features of atomic components found within a ligand molecule and protein molecule (eg, charge, size, shape, polarizability, hyprophobicity, etc), and b) quantifying interactions between such features in the ligand molecule, the protein molecule and the protein/ligand complex , as determined using any number of approaches known in the art (eg. molecular mechanics force fields and/or quantum mechanics). Analyzing sturctural and chemical feature complementarity can, for example, be ascertained visually or by scoring functions based on computed ligand-site interactions as implemented in DOCK, GOLD or Flo.

A three dimensional model of Site II can be used to identify structural and chemical features that may be involved in binding of ligands to Site II. Identified structural or chemical features can then be employed to design ligands or modulators of Site II or identify test molecules as ligands or modulators of Site II.

Therefore, the invention provides a method of identifying structural and chemical features comprising identifying structural and chemical features of all or any part of a Site II using a three-dimensional model of all or any part of said Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. Identification of structural and chemical features may be performed by means known in the art, such as through use of DOCK, GOLD or Flo.

Structure-based design often involves modeling. Modeling is the development of a mathematical construct designed to mimic real molecular geometry and behavior in proteins and small molecules. These mathematical constructs include, but are not limited to: energy calculations for a given geometry of a molecule utilizing forcefields or ab initio methods known in the art; energy minimization using gradients of the energy calculated as atoms are shifted so as to produce a lower energy; conformational searching, ie, locating local energy minima; molecular dynamics wherein a molecular system (single molecule or ligand/protein complex) is propagated forward through increments of time according to Newtonian mechanics using techniques known to the art; calculations of molecular properties such as electrostatic fields, hydrophobicity and lipophilicity; calculation of solvent-accessible or other molecular surfaces and rendition of the molecular properties on those surfaces; comparison of molecules using either atom-atom correspondences or other criteria such as surfaces and properties; quantitiative structure-activity relationships in which molecular features or properties dependent upon them are correlated with activity or bio-assay data. A number of computer modeling systems are available in which a sequence and structure (i.e., structure coordinates) of a protein or portion of a protein can be input. Examples of such computer modeling systems include, but are not limited to, InsightII (Accelrys, Inc., San Diego, CA), SYBYL (Tripos Associates, St. Louis, MO), and Flo (Colin McMartin, Thistlesoft, Colebrook, CT). The computer system then generates the structural details of one or more regions in which a potential ligand binds so that complementary structural and chemical features of the

potential ligands can be determined. Design in these modeling systems is generally based upon the compound being capable of structurally and chemically associating with the protein, i.e. have structural and chemical feature complementarity. In addition, the compound must be able to assume a conformation that allows it to associate with the protein. Some modeling and design systems estimate the potential inhibitory or binding effect of a potential modulator prior to actual synthesis and testing. Using modeling, compounds may be designed *de novo* using an empty binding site. Alternatively, compounds may be designed including some portion of a known ligand, i.e. grown in place. The known ligand may have been determined through virtual screening. Programs for design include, but are not limited to LUDI (Bohm 1992), LeapFrog (Tripos Associates, St. Louis MO) and DOCK (Kuntz et. al., 1982).

Therefore, the invention provides a method of designing a ligand of Site II comprising: (a) modeling all or any part of a Site II; and (b) based on said modeling, designing a chemical entity that has structural and chemical feature complementarity with all or any part of said Site II; wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. The chemical entity is designed to fit spatially into all or any part of the cavity circumscribed by Site II. The chemical entity may be designed manually without the aid of computer software, either *de novo* or including some portion of a known ligand. The chemical entity may be designed by computer either *de novo* or including some portion of a known ligand. Design by computer may employ a database from which chemical entities are chosen based on the model. The method may further comprise: (c) docking the chemical entity into all or any part of the cavity circumscribed by said Site II; and (d) analyzing structural and chemical feature complementarity of the chemical entity with all or any part of said Site II. The method may further comprise analyzing structural and chemical feature complementarity of a second chemical entity with all or any part of said Site II, such as when the modeling operation grows a ligand in place.

The invention also provides a method of designing a modulator of an NHR comprising: (a) modeling all or any part of a Site II; and (b) based on said modeling, designing a chemical entity that has structural and chemical feature complementarity with all or any part of said Site II; wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I. The chemical entity is designed to fit spatially into all or any part of the cavity circumscribed by said Site II. The chemical entity may be designed manually without the aid of computer software, either *de novo* or including some portion of a known ligand. The chemical entity may be designed by computer either *de novo* or including some portion of a known ligand. Design by computer may employ a database from which chemical entities are chosen based on the model. The method may further comprise: (c) docking the chemical entity into all or any part of the cavity circumscribed by said Site II; and (d) analyzing structural and chemical feature complementarity of the chemical entity with all or any part of said Site II. The method may further comprise analyzing structural and chemical feature complementarity of a second chemical entity with all or any part of said Site II, such as when the modeling operation grows a ligand in place.

Virtual screening methods, i.e. methods of evaluating the potential of chemical entities to bind to a given protein or portion of a protein, are well known in the art. These methods often utilize databases as sources of the chemical entities and often are employed in designing ligands. Often these methods begin by visual inspection of the binding site on the computer screen. Selected chemical entities can then be placed, i.e. docked, in one or more positions and orientations within the binding site and chemical and structural feature complementarity can be analyzed.

In virtual screening, molecular docking can be accomplished using software such as InsightII, ICM (Molsoft LLC, La Jolla, CA), and SYBYL, followed by energy minimization and molecular dynamics with standard molecular mechanics forcefields such as CHARMM and MMFF. Examples of computer programs which assist in the selection of chemical entities useful in the present invention include, but are not

limited to, GRID (Goodford, 1985), AUTODOCK (Goodsell, 1990), and DOCK (Kuntz *et. al.* 1982). Databases of chemical entities that may be used include, but are not limited to, ACD (Molecular Designs Limited), Aldrich (Aldrich Chemical Company), NCI (National Cancer Institute), Maybridge(Maybridge Chemical Company Ltd), CCDC (Cambridge Crystallographic Data Center), CAST (Chemical Abstract Service) and Derwent (Derwent Information Limited).

For example, programs such as DOCK (Kuntz *et. al.* 1982) can be used with the structure coordinates of Site II to identify chemical entities from databases or virtual databases of small molecules. These molecules may therefore be suitable candidates for synthesis and testing. Such a virtual screening approach may include, but is not limited to, the following steps:

1) Selection of a chemical entity from a database or elsewhere and positioning the chemical entity in one or more orientations within all or any part of the cavity circumscribed by Site II, wherein Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I.
2) Characterization of the structural and chemical features of the chemical entity and binding site, such as van der Waals interactions, hydrogen bonding interactions, charge interaction, hydrophobic bonding interaction, and dipole interactions
3) Optionally, selection from a database or elsewhere of a chemical entity which can be joined to or replace the docked chemical entity and fit spatially into all or any part of the cavity circumscribed by Site II
4) Evaluation of the docked chemical entity using a combination of scoring schemes which account for van der Waals interactions, hydrogen bonding interactions, charge interaction and hydrophobic

interactions, i.e. evaluation of structural and chemical feature complementarity.

Upon selection of preferred chemical entities, their relationship to each other and Site II can be visualized and then assembled into a single potential ligand. Programs useful in assembling the individual chemical entities include, but are not limited to, SYBYL and LeapFrog (Tripos Associates, St. Louis MO), LUDI (Bohm 1992) and 3D Database systems (Martin 1992).

Thus the invention provides a method for evaluating the potential of a chemical entity to bind to all or any part of Site II comprising: a) docking a chemical entity into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; and b) analyzing structural and chemical feature complementarity between the chemical entity and all or any part of said Site II. The chemical entity may be selected from a database. The method may further comprise a step in which a second chemical entity is joined to the first chemical entity that was docked and analyzed, and the resultant chemical entity is docked and analyzed.

Ligands designed or identified using the methods described herein can then be synthesized and screened in an NHR Site II binding assay (such as is described in Examples 15 and 18), or in an assay designed to test functional activity (such as the cellular tranrepressional assay described in Example 3 and the cellular transcriptional assay described in Example 4, and the competition assays described in Examples 11 and 12). Examples of assays useful in screening of potential ligands or modulators include, but are not limited to, screening in silico, *in vitro* assays and high throughput assays.

Similarly and further to the method for evaluating the potential of a chemical entity to bind Site II, test molecules may be screened, using computational means and biological assays, to identify ligands of Site II and modulators of NHRs.

Thus, the invention provides a method for identifying a modulator of an NHR. The method comprises the following steps, which are preferably, but not necessarily, performed in the order given: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in a biological assay of modulation of an NHR. A test molecule is identified as a modulator of an NHR if the structural and chemical feature complementarity and/or the modulation exceed a desired level. A compound which stimulates or inhibits a measured activity in a cellular assay by greater than 10% is a preferred modulator. The method may further comprise one or more of the following steps: d) screening the test molecule in an assay that characterizes binding to a Site II; and e) screening the test molecule in an assay that characterizes binding to Site I.

A biological assay of modulation of an NHR includes, but is not limited to: a transrepression assay, such as described in Example 3; a transactivation assay, such as described in Example 4; a transrepression competition assay, such as described in Example 11; and a transactivation competition assay, such as described in Example 12. An assay that characterizes binding to Site II includes, but is not limited to, any of the assays described in Examples15 and 18.

The invention provides a method for identifying a ligand of Site II. The method comprises the following steps, which are preferably, but not necessarily, performed in the order given: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing structural and chemical feature complementarity

between the test molecule and all or any part said Site II; and c) screening the test molecule in an assay that characterizes binding to a Site II. A test molecule that binds to Site II is identified as a ligand of Site II. The method may further comprise one or more of the following steps: d) screening the test molecule in a biological assay of modulation of an NHR; and e) screening the test molecule in an assay that characterizes binding to Site I.

In the above-described method of identifying a modulator of an NHR and method of identifying a ligand of Site II, the structure coordinates of a Site II of a first NHR may be used, while the biological assays (i.e. biological assay of modulation of an NHR, or assay that characterizes binding to Site II, or assay that characterizes binding to Site I) may be performed using a second NHR. Preferably, the structure coordinates of a Site II are of the same NHR as the NHR used in the biological assays.

In the present methods, a modulator of an NHR can induce one or more of the following four activities in the NHR. This list is not meant to be inclusive. (1) A modulator of an NHR can induce transrepression. (2) A modulator of an NHR can induce transactivation. (3) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transrepression. (4) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transactivation.

Preferably said modulator of an NHR is a modulator of an SHR, more preferably a modulator of GR.

A modulator of an NHR, SHR or GR that induces transrepression includes, but is not limited to, a dissociated compound.

Preferably said modulator of an NHR induces transrepression. More preferably said modulator of an NHR is a dissociated compound. More preferably said modulator of an NHR is an SHR dissociated compound. Most preferably said modulator of an NHR is a GR dissociated compound.

"All or any part of the cavity circumscribed by Site II" preferably relates to enough of the cavity so as to be useful in docking or modeling a ligand into the cavity. Preferably, all or any part of the cavity is circumscribed by one or more of the following residues: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Q615, P625, Y663, L664 and K667. These are the residues of Site II

that are not also part of Site I. Preferably, all or any part of the cavity is circumscribed by at least four amino acid residues, more preferably at least five amino acids, more preferably at least eight amino acid residues, more preferably at least fifteen amino acid residues, more preferably at least twenty amino acid residues, more preferably at least twenty-five amino acid residues, most preferably at least thirty amino acid residues.

The structure coordinates of Site II of a first NHR may be used in the above methods when one is interested in a second NHR. For instance, one may use the structure coordinates of GR Site II in a method when the end goal is to evaluate the potential of a chemical entity to bind to Site II of another NHR, for instance, androgen receptor. This is because, based on the structural similarity amongst various NHRs, it is possible that a modulator of GR Site II, or structural variants of a modulator of GR Site II, could bind to Site II in other NHRs. It is known in the art that a single steroid can bind to multiple NHRs. For example, cortisol can bind not only to GR but to the mineralocorticoid receptor as well. It is thought that this binding of cortisol occurs via Site I.

Ligands of Site II, and Modulators of NHRs

We have identified Site II in NHRs and identified ligands of Site II as modulators of NHRs and thus drug candidates.

Therefore, the invention provides a ligand of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I.

A ligand can be identified by any art-recognized assay for binding to Site II, such as the assays described in Examples 15 and 18.

Preferred ligands have been identified according to a method of the invention described herein. That is, preferred ligands were identified by a method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe

conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in an assay that characterizes binding to a Site II. A test molecule that binds to Site II is identified as a ligand of Site II. The method may further comprise one or more of the following steps: d) screening the test molecule in a biological assay of modulation of an NHR; and e) screening the test molecule in an assay that characterizes binding to Site I.

Preferred ligands are ligands of an NHR Site II, more preferably of an SHR Site II, most preferably of a GR Site II.

The invention also provides a modulator of an NHR identified according to a method of the invention described herein. That is, the invention provides a modulator of an NHR, wherein said modulator has been identified by a method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in a biological assay of modulation of an NHR. A test molecule is identified as a modulator of an NHR if the structural and chemical feature complementarity and the modulation exceed a desired level. The method may further comprise one or more of the following steps: d) screening the test molecule in an assay that characterizes binding to a Site II; and e) screening the test molecule in an assay that characterizes binding to Site I.

Preferably said modulator of an NHR is a ligand of Site II. Preferred modulators are modulators of an NHR, more preferably of an SHR, most preferably of a GR.

The invention also provides a modulator of an NHR that is a ligand of a Site II. A modulator of an NHR that is a ligand of Site II is part of the invention regardless of how the modulator was identified.

As previously stated, the term "modulator," as used herein, refers to a molecule whose presence induces an activity in the molecule that it modulates. The following information on modulators applies to all of the present inventions.

A modulator can bind to the molecule that it modulates, i.e. be a ligand of the molecule it modulates. A preferred modulator is a ligand of the molecule that it modulates. In the present inventions, a preferred modulator is a ligand of Site II. Modulators include, but are not limited to, small organic molecules, chemical compounds, peptides, peptidomimetics (eg., cyclic peptides, peptide analogs, or constrained peptides) and nucleic acids. Modulators can be natural or synthetic. Preferred modulators are small organic molecules.

A modulator of an NHR can induce one or more of the following four activities in the NHR. This list is not meant to be inclusive. (1) A modulator of an NHR can induce transrepression. (2) A modulator of an NHR can induce transactivation. (3) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transrepression. (4) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transactivation.

One type of modulator of an NHR is one that induces transrepression. Examples of this type of modulator are steroids (such as glucocorticoids and dexamethasone) and dissociated compounds, both of which are discussed further below. Several such modulators are described in the Examples. Such a modulator is useful in treating inflammatory and immune associated diseases and disorders. A modulator that induces tranrespression and synergizes (i.e. has an additive effect) with another modulator that induces transrepression, such as described in Examples 11 and 17, is included in the definition of a modulator that induces transrepression.

Another type of modulator is a dissociated compound. A dissociated compound is a modulator that induces transrepression while inducing none or

minimal transactivation. That is, a dissociated compound induces activity (1) above but induces no or little activity (2) above. Several such modulators are described in the Examples. A dissociated compound also may inhibit or antagonize the ability of another modulator from causing transactivation, i.e. a dissociated compound may cause activity (4) above, such as the compound described in Examples 11 and 12, Dissociated compounds that induce AP-1 and NF-κB inhibitory activity without causing DNA-binding activity are useful in treating inflammatory and immune associated diseases and disorders, such as in immunosuppressive therapy. AP-1 and NF-κB are transcription factors which regulate the expression of a large number of genes involved in immune and inflammatory responses. These genes include TNF-alpha, IL-2, IL-5, E-selectin, Eoxtaxin, Rantes, Cox-2, among others. By way of example, glucocorticoids, which inhibit the activity of both AP-1 and NF-κB are one of the most potent anti-inflammatory drugs known to date. Glucocorticoids are used to treat more than 50 diseases, however, their use in patients is often limited by the side effects of osteoporosis, diabetes, glaucoma, muscle loss, facial swelling, personality changes, and others. It is thought that a compound which inhibits NF-κB and AP-1 without inducing DNA binding (i.e. without causing transactivation) would possess most of the anti-inflammatory effects of glucocorticoids without the side effects.

Another type of modulator of is one that induces transactivation without inducing transrepression. In the case of GR, such a modulator that induces DNA binding and transcription may be useful in treating Addison's disease or other metabolic disorders where circulating glucocorticoid levels are lower than normal and where causing transrepression is not desireable.

Another type of modulator is one that induces both transrepression and transactivation. Examples of this type of modulator are steroids such as glucocorticoids and dexamethasone. Such a modulator is useful in treating inflammatory and immune associated diseases and disorders.

Another type of modulator is one that antagonizes a modulator that induces transactivation. These modulators inhibit transcription. Such a modulator is described in Example 12. These modulators may also induce transrepression. In the case of GR, a modulator that antagonizes a modulator that induces transactivation

may be useful in treating metabolic diseases such as diabetes, hypertension, obesity, glaucoma, depression, and AIDS, and in wound healing. It is believed that some of these diseases are, at least in part, caused by higher than normal circulating levels of glucocorticoids. Inhibiting the transactivation or DNA binding induced by the increased circulating glucocorticoids may ameliorate or attenuate some or all of these diseases. Preferably, the GR modulator that antagonizes a modulator that induces transactivation does not also induce transrepression.

All modulators of NHRs and ligands of Site II may be useful in elucidating the mechanism of transcriptional regulation mediated by NHRs. These modulators and ligands could be used in cellular and animal studies to determine the requirement for NHRs in the induction or inhibition of gene expression, the association of coactivators and corepressors with NHRs, and the role of chaperones in regulating NHR activity, among other experiments.

Modulators of NHRs may be found by performing any art-recognized transrepression assay, transactivation assay, transrepression competition assay, or transactivation competition assay. Such assays include, but are not limited to, the assays described in Examples 3, 4, 11 and 12.

For a modulator of an NHR that induces transrepression, such as and including a dissociated compound, a preferred modulator induces transrepression at an IC50 of between 0.1 nM and 10 μM, more preferably between 0.1 nm and 1 μM (such as between 33 nM and 275 nM, or between 15 nm and 275 nm), more preferably between 0.1 nM and 100 nM, most preferably between 0.1 nM and 10 nM. Transrepression may be measured by any art-recognized method, such as the cellular transrepressional assays described in Example 3. An IC50 is the modulator concentration which causes a 50% repression of transcription.

For a modulator of an NHR that induces none to minimal transactivation, such as and including a dissociated compound, a preferred modulator induces transactivation at an EC50 of greater than 1nM, preferably at greater than 100nM, more preferably at greater than 1 μM, and most preferably at greater than 40 μM. Transactivation may be measured by any method known in the art, such as the cellular transcriptional assays described in Example 4. An EC50 is modulator concentration required to cause a 50% stimulation of transcription.

For a dissociated compound, a preferred dissociated compound has a dissociation constant of greater than 0.1, more preferably greater than 10, more preferably greater than 100 (such as between 167 and 1000, or between 137 and 1000), most preferably greater than 1000. The dissociation constant is calculated by dividing the EC50 for transactivation by the IC50 for transrepression.

For a modulator of an NHR that antagonizes a modulator that induces transactivation, a preferred modulator antagonizes at an IC50 of between 0.1 nM and 10 μM, more preferably between 0.1 nM and 1 μM, more preferably between 0.1 nM and 100 nM, most preferably between 0.1 nM and 10 nM.

For a modulator of an NHR that induces transactivation, a preferred modulator induces transactivation at an IC50 of between 0.1 nM and 10 μM, more preferably between 0.1 nM and 1 μM, more preferably between 0.1 nM and 100 nM, most preferably between 0.1 nM and 10 nM.

Methods of Modulating a Nuclear Hormone Receptor

The modulators of the present invention may be used to modulate an NHR.

Thus, the invention provides a method of modulating an NHR comprising administering a modulator of an NHR in an amount sufficient to modulate the NHR, wherein said modulator of an NHR is a ligand of a Site II or was identified by a method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in a biological assay of modulation of an NHR. A test molecule is identified as a modulator of an NHR if the structural and chemical feature complementarity and the modulation exceed a desired level. The method may further comprise one or more of the following steps: d) screening the test molecule in an assay that characterizes

binding to a Site II; and e) screening the test molecule in an assay that characterizes binding to Site I.

The invention provides a method of inducing transrepression comprising administering a modulator of an NHR in an amount sufficient to cause transrepression, wherein said modulator on an NHR is a ligand of Site II or was identified by the method described above.

The invention provides a method of inhibiting AP-1-dependent gene expression comprising administering a modulator of an NHR in an amount sufficient to inhibit AP-1-dependent gene expression, wherein said modulator on an NHR is a ligand of Site II or was identified by the method described above.

The invention provides a method of inhibiting NF-κB-dependent gene expression comprising administering a modulator of an NHR in an amount sufficient to inhibit NF-κB -dependent gene expression, wherein said modulator on an NHR is a ligand of Site II or was identified by the method described above.

The invention provides a method of antagonizing transactivation comprising administering a modulator of an NHR in an amount sufficient to antagonize transactivation, wherein said modulator on an NHR is a ligand of Site II or was identified by the method described above.

Preferred ligands used in the methods of the present invention were identified by a method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in an assay that characterizes binding to a Site II. A test molecule that binds to Site II is identified as a ligand of Site II. The method may further comprise one or more of the following steps: d) screening the test molecule in a biological assay of modulation of an NHR; and e) screening the test molecule in an assay that characterizes binding to Site I.

The methods may be practiced *in vitro* or *in vivo*. When practiced in vitro, the method may employ any number of art-recognized *in vitro* systems, including the assays described in Examples 3 and 4. *In vivo* methods include, but are not limited to, any of the ways described in the section below on methods of treatment.

Pharmaceutical Compositions

The invention provides a pharmaceutical composition comprising: (a) a modulator of an NHR that was identified by a method comprising: (i) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; (ii) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and (iii) screening the test molecule in a biological assay of modulation of an NHR; and (b) a pharmaceutically acceptable carrier, adjuvant, excipient or vehicle. A test molecule is identified as a modulator of an NHR if the structural and chemical feature complementarity and the modulation exceed a desired level. The method used to identify a modulator of Site II may further comprise one or more of the following steps: d) screening the test molecule in an assay that characterizes binding to a Site II; and e) screening the test molecule in an assay that characterizes binding to Site I.

The invention provides a pharmaceutical composition comprising a modulator of an NHR that is a ligand of Site II and a pharmaceutically acceptable carrier, adjuvant, excipient or vehicle. Preferred ligands of Site II were identified by a method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-

W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in an assay that characterizes binding to a Site II. A test molecule that binds to Site II is identified as a ligand of Site II. The method may further comprise one or more of the following steps: d) screening the test molecule in a biological assay of modulation of an NHR; and e) screening the test molecule in an assay that characterizes binding to Site I.

In the present pharmaceutical compositions, a modulator of an NHR can induce one or more of the following four activities in the NHR. This list is not meant to be inclusive. (1) A modulator of an NHR can induce transrepression. (2) A modulator of an NHR can induce transactivation. (3) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transrepression. (4) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transactivation.

Preferably said modulator of an NHR is a modulator of an SHR, more preferably a modulator of GR.

A modulator of an NHR, SHR or GR that induces transrepression includes, but is not limited to, a dissociated compound.

Preferably said modulator of an NHR induces transrepression. More preferably said modulator of an NHR is a dissociated compound. More preferably said modulator of an NHR is an SHR dissociated compound. Most preferably said modulator of an NHR is a GR dissociated compound.

The pharmaceutical composition may further comprise at least one additional therapeutic agent. "Additional therapeutic agents" encompasses, but is not limited to, an agent or agents selected from the group consisting of an immunosuppressant, an anti-cancer agent, an anti-viral agent, an anti-inflammatory agent, an anti-fungal agent, an antibiotic, an anti-vascular hyperproliferation compound, an anti-diabetic agent, or an anti-depressant agent.

The term "pharmaceutically acceptable carrier, adjuvant or vehicle" refers to a carrier, adjuvant or vehicle that may be administered to a subject, together with a modulator of the present invention, and which does not destroy the pharmacological

activity thereof. Pharmaceutically acceptable carriers, adjuvants and vehicles that may be used in the pharmaceutical compositions of the present invention include, but are not limited to, the following: ion exchangers, alumina, aluminum stearate, lecithin, self-emulsifying drug delivery systems ("SEDDS") such as d(-tocopherol polyethyleneglycol 1000 succinate), surfactants used in pharmaceutical dosage forms such as Tweens or other similar polymeric delivery matrices, serum proteins such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts or electrolytes such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol and wool fat. Cyclodextrins such as α-, β- and γ-cyclodextrin, or chemically modified derivatives such as hydroxyalkylcyclodextrins, including 2- and 3-hydroxypropyl-β-cyclodextrins, or other solubilized derivatives may also be used to enhance delivery of the modulators of the present invention.

The compositions of the present invention may contain other therapeutic agent(s) as described below, and may be formulated, for example, by employing conventional solid or liquid vehicles or diluents, as well as pharmaceutical additives of a type appropriate to the mode of desired administration (for example, excipients, binders, preservatives, stabilizers, flavors, etc.) according to techniques such as those well known in the art of pharmaceutical formulation.

The modulators may be administered by any suitable means, for example, orally, such as in the form of tablets, capsules, granules or powders; sublingually; buccally; parenterally, such as by subcutaneous, intravenous, intramuscular, or intrasternal injection or infusion techniques (e.g., as sterile injectable aqueous or non-aqueous solutions or suspensions); nasally such as by inhalation spray; topically, such as in the form of a cream or ointment; or rectally such as in the form of suppositories; in dosage unit formulations containing non-toxic, pharmaceutically acceptable vehicles or diluents. The present modulators may, for example, be administered in a form suitable for immediate release or extended release. Immediate release or

extended release may be achieved by the use of suitable pharmaceutical compositions comprising the present modulators, or, particularly in the case of extended release, by the use of devices such as subcutaneous implants or osmotic pumps. The present modulators may also be administered liposomally.

Exemplary compositions for oral administration include suspensions which may contain, for example, microcrystalline cellulose for imparting bulk, alginic acid or sodium alginate as a suspending agent, methylcellulose as a viscosity enhancer, and sweeteners or flavoring agents such as those known in the art; and immediate release tablets which may contain, for example, microcrystalline cellulose, dicalcium phosphate, starch, magnesium stearate and/or lactose and/or other excipients, binders, extenders, disintegrants, diluents and lubricants such as those known in the art. The present modulators may also be delivered through the oral cavity by sublingual and/or buccal administration. Molded tablets, compressed tablets or freeze-dried tablets are exemplary forms which may be used. Exemplary compositions include those formulating the present modulator(s) with fast dissolving diluents such as mannitol, lactose, sucrose and/or cyclodextrins. Also included in such formulations may be high molecular weight excipients such as celluloses (avicel) or polyethylene glycols (PEG). Such formulations may also include an excipient to aid mucosal adhesion such as hydroxy propyl cellulose (HPC), hydroxy propyl methyl cellulose (HPMC), sodium carboxy methyl cellulose (SCMC), maleic anhydride copolymer (e.g., Gantrez), and agents to control release such as polyacrylic copolymer (e.g., Carbopol 934). Lubricants, glidants, flavors, coloring agents and stabilizers may also be added for ease of fabrication and use.

Exemplary compositions for nasal aerosol or inhalation administration include solutions in saline which may contain, for example, benzyl alcohol or other suitable preservatives, absorption promoters to enhance bioavailability, and/or other solubilizing or dispersing agents such as those known in the art.

Exemplary compositions for parenteral administration include injectable solutions or suspensions which may contain, for example, suitable non-toxic, parenterally acceptable diluents or solvents, such as mannitol, 1,3-butanediol, water, Ringer's solution, an isotonic sodium chloride solution, or other suitable dispersing or wetting and suspending agents, including synthetic mono- or diglycerides, and fatty

acids, including oleic acid. The term "parenteral" as used herein includes subcutaneous, intracutaneous, intravenous, intramuscular, intraarticular, intraarterial, intrasynovial, intrasternal, intrathecal, intralesional and intracranial injection or infusion techniques.

Exemplary compositions for rectal administration include suppositories which may contain, for example, a suitable non-irritating excipient, such as cocoa butter, synthetic glyceride esters or polyethylene glycols, which are solid at ordinary temperatures, but liquify and/or dissolve in the rectal cavity to release the drug.

Exemplary compositions for topical administration include a topical carrier such as Plastibase (mineral oil gelled with polyethylene).

The effective amount of a modulator of the present invention may be determined by one of ordinary skill in the art, and includes exemplary dosage amounts for an adult human of from about 0.1 to 500 mg/kg of body weight of active modulator per day, which may be administered in a single dose or in the form of individual divided doses, such as from 1 to 5 times per day. It will be understood that the specific dose level and frequency of dosage for any particular subject may be varied and will depend upon a variety of factors including the activity of the specific modulator employed, the metabolic stability and length of action of that modulator, the species, age, body weight, general health, sex and diet of the subject, the mode and time of administration, rate of excretion, drug combination, and severity of the particular condition. Preferred subjects for treatment include animals, most preferably mammalian species such as humans, and domestic animals such as dogs, cats and the like, subject to NHR-associated diseases.

The modulators of the present invention may be employed alone or in combination with each other and/or other suitable therapeutic agent(s) useful in the treatment of NHR-associated diseases, such as immunosuppressants, anti-cancer agents, anti-viral agents, anti-inflammatory agents, anti-fungal agents, antibiotics, anti-vascular hyperproliferation agents, anti-diabetic agents, or anti-depressant agents. Such other therapeutic agent(s) may be administered prior to, simultaneously with or following the administration of the compound(s) of the present invention.

Exemplary such other therapeutic agents include the following: cyclosporins (e.g., cyclosporin A), CTLA4-Ig, antibodies such as anti-TNF-α (such as Remicade),

anti-ICAM-3, anti-IL-2 receptor (Anti-Tac), anti-CD45RB, anti-CD2, anti-CD3 (OKT-3), anti-CD4, anti-CD80, anti-CD86, monoclonal antibody OKT3, agents blocking the interaction between CD40 and CD154 (a.k.a. "gp39"), such as antibodies specific for CD40 and/or CD154, fusion proteins constructed from CD40 and/or CD154/gp39 (e.g., CD40Ig and CD8gp39), inhibitors, such as nuclear translocation inhibitors, of NF-κB function, such as deoxyspergualin (DSG), non-steroidal antiinflammatory drugs (NSAIDs) such as ibuprofen, celecoxib, rofecoxib, cox-2 inhibitors, and aspirin, antibiotics such as penicillin, and tetracycline, steroids such as prednisone or dexamethasone, gold compounds, antiviral agents such as abacavir, antiproliferative agents such as mycophenolate, 5-fluorouracil, cisplatin, methotrexate, leflunomide, FK506 (tacrolimus, Prograf), cytotoxic drugs such as azathiprine and cyclophosphamide, TNF-α inhibitors such as tenidap, anti-TNF antibodies (such as Remicade) or soluble TNF receptor (such as Enbrel), and rapamycin (sirolimus or Rapamune) or derivatives thereof. The above other therapeutic agents, when employed in combination with the modulators of the present invention, may be used, for example, in those amounts indicated in the Physicians' Desk Reference (PDR) or as otherwise determined by one of ordinary skill in the art.

Methods of Treatment

The modulators of the present invention may be used to treat diseases.

The present invention provides a method of treating an NHR-associated disease comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR, wherein said modulator of an NHR was identified by the method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in a biological assay of modulation of an NHR. A test

molecule is identified as a modulator of an NHR if the structural and/or chemical feature complementarity and the modulation exceed a desired level. The method may further comprise one or more of the following steps: d) screening the test molecule in an assay that characterizes binding to a Site II; and e) screening the test molecule in an assay that characterizes binding to Site I.

The present invention provides a method of treating an NHR-associated disease comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that is a ligand of a Site II.

Preferably said NHR-associated disease is an SHR-associated disease and said modulator of an NHR is a modulator of an SHR. Most preferably said NHR-associated disease is a GR-associated disease and said modulator of an NHR is a modulator of GR.

The present invention provides a method of treating a disease associated with NHR transactivation comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR, wherein said modulator of an NHR was identified by the method described above.

The present invention provides a method of treating a disease associated with NHR transactivation comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that is a ligand of a Site II.

The present invention provides a method of treating a disease associated with NHR transrepression comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR, wherein said modulator of an NHR was identified by the method described above.

The present invention provides a method of treating a disease associated with NHR transrepression comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that is a ligand of a Site.

The invention provides a method of treating a disease associated with AP-1-dependent gene expression or NF-κB-dependent gene expression comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR, wherein said modulator of an NHR was identified by the method described above.

The invention provides a method of treating a disease associated with AP-1-dependent gene expression or NF-κB-dependent gene expression comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that is a ligand of a Site II.

The invention provides a method of treating an inflammatory or immune associated disease or disorder comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR, wherein said modulator of an NHR was identified by the method described above.

The invention provides a method of treating an inflammatory or immune disease or disorder comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that is a ligand of a Site II.

Preferably said methods of treating an inflammatory or immune disease or disorder comprise inhibiting AP-1-dependent gene expression or NF-κB-dependent gene expression by administering said modulator of an NHR in an amount effective to inhibit AP-1-dependent gene expression or NF-κB-dependent gene expression.

The present invention provides a method of treating a disease treatable by inducing NHR transrepression comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that induces transrepression, wherein said modulator of an NHR was identified by the method described above.

The present invention provides a method of treating a disease treatable by inducing NHR transrepression comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that induces transrepression, wherein said modulator of an NHR is a ligand of a Site II.

The present invention provides a method of treating a disease treatable by antagonizing NHR transactivation comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR that antagonizes transactivation, wherein said modulator of an NHR was identified by the method described above.

The present invention provides a method of treating a disease treatable by antagonizing NHR transactivation comprising administering to a subject in need

thereof, in an amount effective therefore, at least one modulator of an NHR that antagonizes transactivation, wherein said modulator of an NHR is a ligand of a Site II.

Preferred ligands of Site II used in the present methods of treatment were identified by a method comprising: a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; b) analyzing the structural and chemical feature complementarity between the test molecule and all or any part said Site II; and c) screening the test molecule in an assay that characterizes binding to a Site II. A test molecule that binds to Site II is identified as a ligand of Site II. The method may further comprise one or more of the following steps: d) screening the test molecule in a biological assay of modulation of an NHR; and e) screening the test molecule in an assay that characterizes binding to Site I.

A preferred ligand of Site II was identified by screening a test molecule in an assay that characterizes binding to Site II.

Preferably said NHR is an SHR, more preferably a GR.

In the present methods of treatment, a modulator of an NHR can induce one or more of the following four activities in the NHR. This list is not meant to be inclusive. (1) A modulator of an NHR can induce transrepression. (2) A modulator of an NHR can induce transactivation. (3) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transrepression. (4) A modulator of an NHR can inhibit or antagonize the ability of another modulator from inducing transactivation.

Preferably said modulator of an NHR is a modulator of an SHR, more preferably a modulator of GR.

A modulator of an NHR, SHR or GR that induces transrepression includes, but is not limited to, a dissociated compound.

Preferably said modulator of an NHR induces transrepression. More preferably said modulator of an NHR is a dissociated compound. More preferably

said modulator of an NHR is an SHR dissociated compound. Most preferably said modulator of an NHR is a GR dissociated compound.

Preferably said subject is a mammal, most preferably a human.

Other therapeutic agent(s), such as those described above in the section on pharmaceutical compositions, may be employed with the modulators in the present methods. In the methods of the present invention, such other therapeutic agent(s) may be administered prior to, simultaneously with or following the administration of the compound(s) of the present invention.

Modes of administration useful in the present invention are described above in the section of pharmaceutical compositions.

In a particular embodiment, the modulators of the present invention are useful for the treatment of the aforementioned exemplary disorders irrespective of their etiology, for example, for the treatment of transplant rejection, rheumatoid arthritis, inflammatory bowel disease, and viral infections.

Methods of Designing Mutants

We have identified Site II in NHRs as a binding site whose ligands modulate NHRs. Now that Site II is known to be a region of interest, mutants of NHRs, and mutants of portions of NHRs, in which Site II is mutated may be made.

Thus, the invention provides a method of designing a mutant comprising making one or more amino acid mutations in a Site II. The mutant so designed may be an NHR or a portion of an NHR, such as the LBD.

Preferably the mutation(s) is a deletion or substitution of one or more of the amino acids of said Site II. When the mutation(s) is an amino acid insertion, preferably the amino acid(s) inserted are inserted next to an amino acid of said Site II.

Preferably a mutation involves one or more of the following amino acids in human GR: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Q615, P625, Y663, L664 and K667, or one or more of the corresponding amino acids in another NHR or non-human GR as can be seen in Figures 2 and 6 respectively. Preferably a mutation involves one or more of the following amino acids in human GR: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Y663, L664 and K667, or one or more of the corresponding amino acids

in another NHR or non-human GR as can be seen in Figures 2 and 6 respectively. Preferably the deletion or substitution is of one or more of the aforementioned amino acids or corresponding amino acids, and preferably the insertion is next to one or more the aforementioned amino acids or corresponding amino acids.

The method may further comprise using all or part of a model of a Site II to visualize all or part of Site II in its mutated or native form. Preferably said model is a three-dimensional model.

Mutation includes one or more amino acid deletions, insertions, inversions, repeats, or substitutions as compared to the native protein. Various methods of making mutations are known to one of ordinary skill in the art. A mutant may have the same, similar, or altered activity as compared to the native protein. Activity refers to transrepression, transactivation, and ligand binding. Preferred mutants have at least 25% sequence identity, more preferably 50% sequence identity, more preferably 75% sequence identity, and most preferably 95% sequence identity to the native protein.

A mutant designed by the method of the invention that has the same or similar biological activity as the native NHR or native portion of NHR may be useful for any purpose for which the native is useful. A mutant designed by the method of the invention that has altered biological activity as the native may be useful in binding assays to test the ability of a potential ligand to bind to or associate with Site II. A mutant designed by the method of the invention that has the altered biological activity from the native may be useful in further elucidating the biological role of Site II.

Example 16 illustrates designing mutants comprising making one or more amino acid mutations in Site II.

Mutants of Site II

The invention provides a mutant NHR, or a mutant portion of an NHR, comprising one or more amino acid mutations in Site II.

Said mutant portion of an NHR preferably comprises a mutant LBD of the NHR, more preferably consists of a mutant LBD of the NHR.

Preferably the mutation(s) is a deletion or substitution of one or more of the amino acids of Site II. When the mutation(s) is an amino acid insertion, preferably the amino acid(s) inserted are inserted next to an amino acid of Site II.

Preferably a mutation involves one or more of the following amino acids in human GR: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Q615, P625, Y663, L664 and K667, or one or more of the corresponding amino acids in another NHR or non-human GR as can be seen in Figures 2 and 6 respectively. Preferably a mutation involves one or more of the following amino acids in human GR: E537-V543, V571-W577, S599-W600, F602-L603, F606-A607, W610, R614, Y663, L664 and K667, or one or more of the corresponding amino acids in another NHR or non-human GR as can be seen in Figures 2 and 6 respectively. Preferably the deletion or substitution is of one or more of the aforementioned amino acids or corresponding amino acids, and preferably the insertion is next to one or more the aforementioned amino acids or corresponding amino acids.

Mutation includes one or more amino acid deletions, insertions, inversions, repeats, or substitutions as compared to the native protein. Various methods of making mutations are known to one of ordinary skill in the art. A mutant may have the same, similar, or altered activity as compared to the native protein. Activity refers to transrepression, transactivation, and ligand binding. Preferred mutants have at least 25% sequence identity, more preferably 50% sequence identity, more preferably 75% sequence identity, and most preferably 95% sequence identity to the native protein.

A mutant of the present invention that has the same or similar biological activity as the native NHR, or native portion of NHR, may be useful for any purpose for which the native is useful. A mutant of the present invention that has altered biological activity as the native may be useful in binding assays to test the ability of a potential ligand to bind to or associate with Site II. A mutant of the present invention that has the altered biological activity from the native may be useful in further elucidating the biological role of Site II.

In preferred mutants, the mutation consists of five or fewer substitutions, more preferably four or fewer substitutions, more preferably three or fewer substitutions, more preferably two or fewer substitutions, most preferably one substitution. A substitution is preferably a conservative amino acid substitution.

In preferred mutants, the mutation consists of three or fewer deletions, more preferably two or fewer deletions, most preferably one deletion.

In preferred mutants, the mutation consists of two or fewer substitutions and two or fewer deletions.

Example 16 illustrates mutants comprising making one or more amino acid mutations in Site II.

Site II Binding Assay

The invention provides a method of measuring the binding of a test molecule to Site II comprising: (a) incubating an NHR with a ligand of Site II and said test molecule; and (b) measuring the ability of said test molecule to compete for binding to said Site II with said ligand; wherein said ability to compete is the measure of binding of said test molecule to Site II. The method may further comprise comparing the ability of said test molecule to modulate a native NHR and to modulate an NHR mutated in Site II.

The ligand of Site II may be identified by any art-recognized method, such as those described in Examples 15 and 16.

The NHR may be in a purified form, in a partially purified form, or in a cell lysate.

In order to measure the ability of said test molecule to compete for binding to Site II with said ligand, the ligand can be labeled, such as radiolabeled or fluorescently labeled. Binding can be measured using any art-recognized technique, such as fluorescence quenching, fluorescence polarization, filter binding, scintillation proximity assay, among others. The ability to compete is determined by comparing the measured value with the labeled compound alone to the measured value in the presence of the unlabeled test molecule. A decrease in the measured signal indicates binding of the test molecule.

The ability of said test molecule to modulate a native NHR and to modulate an NHR mutated in Site II can be determined by measuring transrepression and transactivation using methods such as described in Examples 3 and 4.

One such Site II binding assay is described in Example 18. Example 18 provides a method of measuring the binding of a test molecule to Site II by: incubating said test molecule with an NHR, a Site I ligand (such as FITC-dexamethasone), and a known Site II ligand that inhibits the binding of the Site I

ligand to Site I. A test molecule that does not inhibit the binding of the Site I ligand to Site I and does bind to Site II will displace the known Site II ligand, thus allowing the Site I ligand to bind to Site I. The binding of the Site I ligand to Site I can be measured. The comparison of the Site I ligand binding to Site I in the presence of the Site II ligand with and without the test molecule provides a measurement of relative binding of the test molecule to Site II. In order to measure the ability of said Site I ligand to bind to Site I, the Site I ligand can be labeled, such as radiolabeled or fluorescently labeled. Binding can be measured using any art-recognized technique, such as fluorescence quenching, fluorescence polarization, filter binding, scintillation proximity assay, among others.

Models of Site II

We have identified Site II in NHRs as a binding site whose ligands modulate NHRs. We have focused on Site II as a region of interest in NHRs. Now that Site II is known to be a region of interest, models of Site II, such as three-dimensional models, useful in drug design may be made.

Thus, the invention provides a model comprising all or any part of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I.

In a preferred embodiment the model consists of all or any part of Site II.

In another preferred embodiment the model: (a) comprises all or any part of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; and (b) does not comprise structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of one or more of

amino acids M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748 according to Table I. Preferably, said data does not comprise structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of all of amino acids M560, L563, N564, L608, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748 according to Table I. Preferably, the root mean square deviation of part (b) is less than 1.5 Å, more preferably less that 1.0 Å, yet more preferably less than 0.9, 0.8, 0.7, 0.6 0.5, 0.4, 0.3, 0.2, or 0.1 Å, most preferably 0.0 Å.

A model of a Site II of the present invention may be any type of art-recognized model, including but not limited to: three-dimensional models; and steric/electrostatic field definition models that can be used to study/compute the putative interactions ligands might undergo. A three-dimensional model may be produced through use of structure coordinates, such as are ribbon diagrams.

A three-dimensional model of a Site II of the present invention is useful for designing and identifying ligands and modulators of NHRs.

It should be understood that one skilled in the field is able to make various modifications to the compositions and methods described above, applying the ordinary level of skill in the field, without departing from the spirit or scope of the invention. All such modifications are intended to be included within the invention as defined in the appended claims.

EXAMPLES

The examples below are provided to illustrate the subject invention and are not intended to limit the invention.

Example 1

Compound Synthesis

The fifty-one compounds used in the following examples were synthesized as follows. These compounds and their synthesis are described in the co-pending provisional application entitled "Modulators of the Glucocorticoid Receptor and Method," attorney docket number QA266PSP, U.S. Application No. 60/396,877, filed on July 18, 2002, and in co-pending utility application entitled "Modulators of the

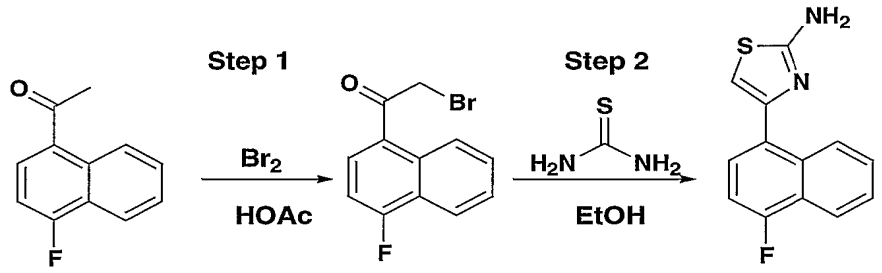
Glucocorticoid Receptor and Method," attorney docket number QA266NP, U.S. Application No._____, filed concurrently herewith. The contents of U.S. Application No. 60/396,877 and QA266NP are incorporated herein by reference in their entirety.

Preparations

The preparations set out below are for the synthesis of reagents that were not obtained from commercial sources and were employed for the preparation of compounds. All chemical structures in the tables and schemes are racemic unless specified otherwise.

Preparation 1

4-[1-(4-Fluoro)naphthyl]aminothiazole 1a



1a

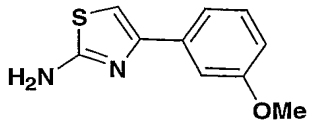
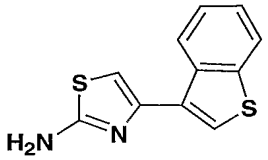
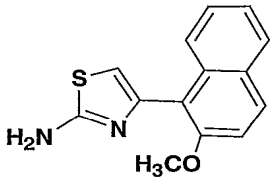
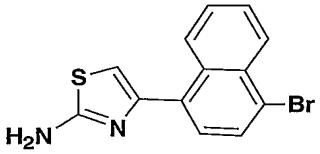
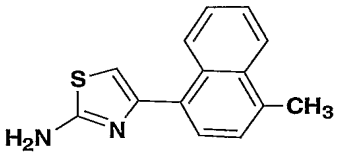
Step 1

To a solution of 4'-fluoro-1'-acetonaphthone (28.69 mmol, 5.4 g) in 1,4-dioxane (18.0 mL) at 0° C was added bromine (35.13 mmol, 5.61 g). After 3 hours at room temperature the reaction mixture was concentrated in vacuo to give 7.66 g (Y: 100%) of the product of step 1.

Step 2

To a solution of the product of step 1 (28.69 mmol, 7.66 g) in ethyl alcohol (20 mL) at room temperature was added thiourea (36.13 mmol, 2.75 g). After 1 hour at room temperature a precipitate formed. To the reaction mixture was added water (100 mL) and the solid was collected by vacuum filtration. The solid was then washed with water (3 x 100 mL) and dichloromethane (3 x 100 mL). The solid was then dried in vacuo to give 5.5 g (Y: 75%) of the title compound 1a. MS (E+) *m/z*: 245 (MH^+).

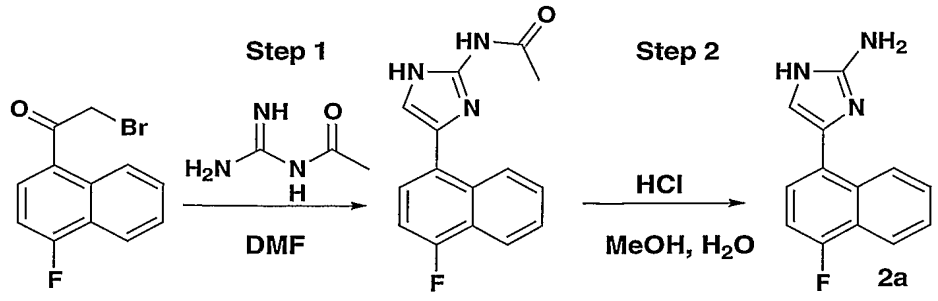
In a similar manner the following compounds were prepared from the corresponding ketone.

Preparation	Structure
1b	
1q	
1r	
1t	
1w	

5

Preparation 2

4-[1-(4-Fluoro)naphthyl]aminoimidazole 2a



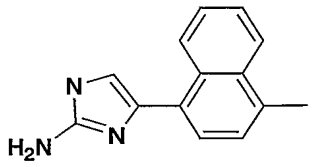
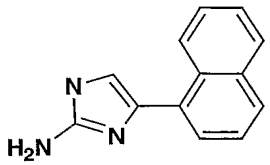
Step 1

To a solution of the product of preparation 1a, step 1 (18.73 mmol, 5.0 g) in DMF (15 mL) at room temperature was added 1-acetylguanidine (57.43 mmol, 5.80 g). After 5 hours at room temperature, the reaction mixture was diluted with water (100 mL) and extracted with ethyl acetate (3 x 100 mL). The organic phases were concentrated in vacuo and the residue chromatographed on silica gel (eluted with 5% methanol in dichloromethane) to give 2.0 g (Y: 39%) of the product of step 1. MS (E+) *m/z*: 270 (MH^+).

Step 2

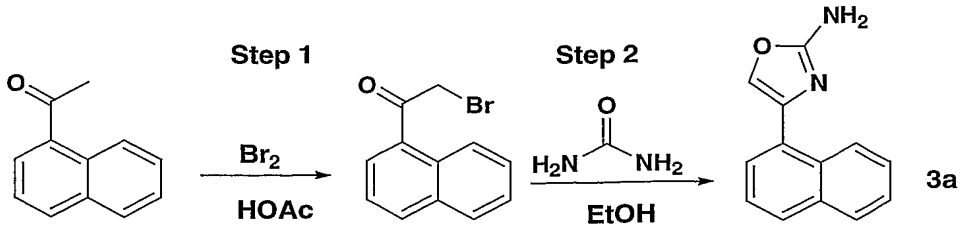
To a solution of the product of step 1 (7.43 mmol, 2.0 g) in methanol (17 mL) was added water (8.5 mL) and 12 N HCl (12.0 mL). After 1 hour at reflux the reaction mixture was concentrated in vacuo to approximately 15 mL. The resulting solution was then purified and neutralized by cation exchange SPE to give 1.66 g (Y: 99%) of the title compound **2a**. MS (E+) *m/z*: 228 (MH^+).

In a similar manner the following compounds were prepared from the corresponding ketones.

Preparation	Structure
2b	
2e	

Preparation 3

4-(1-naphthyl)aminooxazole 3a



Step 1

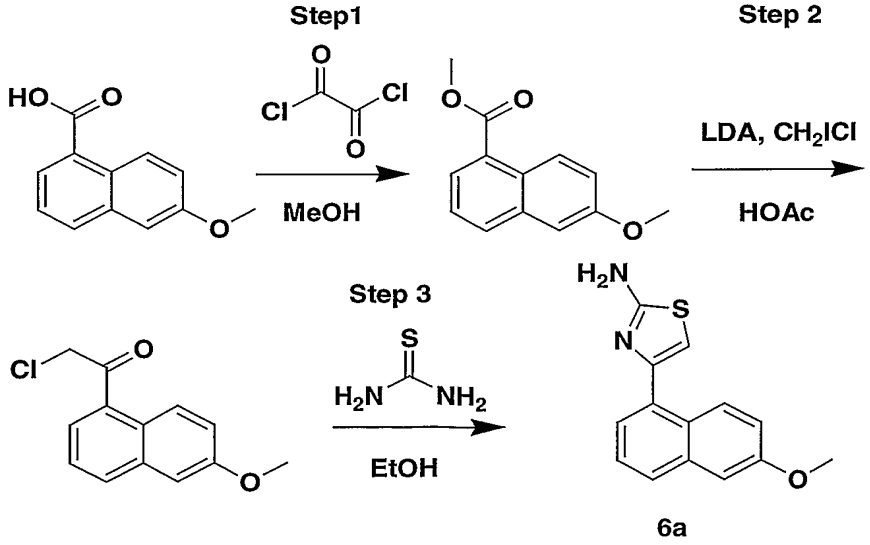
To a solution of 1-acetonaphthone (29.38 mmol, 5.0 g) in glacial acetic acid (10.0 mL) at RT was added bromine (30.06 mmol, 4.80 g) in glacial acetic acid (5.0 mL). After 5 minutes the reaction mixture was poured onto crushed ice and extracted with dichloromethane to give 7.31 g (Y: 100%) of the product of step 1. MS (E+) *m/z*: 250 (MH^+).

Step 2

To a solution of the product of step 1 (5.50 mmol, 1.37 g) in ethyl alcohol (10 mL) was added urea (27.50 mmol, 1.65 g). After 2 hours at reflux the reaction mixture was concentrated in vacuo and the residue chromatographed on silica gel (eluted with 30% ethyl acetate in hexane) to give 100 mg (Y: 9%) of the title compound **3a**. MS (E+) *m/z*: 211 (MH^+).

Preparation 6

4-[1-(6-Methoxy)naphthyl]-3-aminothiazole 6a



Step 1

To a solution of 6-methoxy-1-naphthoic acid (0.5 g, 2.47 mmol, 1.0 equi.) in dichloromethane (10 mL) at room temperature was added a solution of oxalyl chloride (2M in dichloromethane, 2.5 mL, 5.0 mmol, 2 equi.). The solution was stirred at room temperature for 2 hours, and the excess oxalyl chloride removed *in vacuo*. The residue was dissolved in methanol and stirred at room temperature for 18 hours. The solvent was removed *in vacuo*, yielding 0.45 g (84%) of the product of step 1: LC/MS (m/z 217, $(M-H)^+$); ^1H NMR ($CDCl_3$) δ 8.82 (d, 1H), 8.03 (dd, 1H), 7.90 (d, 1H), 7.44 (t, 1H), 7.26 (dd, 1H), 7.16 (s, 1H), 4.02 (s, 3H), 3.95 (s, 3H).

Step 2

Reference: P. Chen, P.T. Cheng, S.H. Spergel, R. Zahler, X. Wang, J. Thottathil, J.C. Barrish, R.P. Polniaszek, *Tetrahedron Letters*, **38**, 3175 (1997).

To a solution of the product of step 1 (0.238 g, 1.1 mmol, 1.0 equi.) and chloroiodomethane (0.32 mL, 4.4 mmol, 4 equi.) in THF (5 mL) was added a solution of LDA (2M, 2.2 mL, 4.0 equi.) in THF (10 mL) dropwise in 30 minutes, while keeping the solution temperature at -78°C. The reaction solution was stirred at -78°C for 10 minutes. A solution of acetic acid (1.5 mL) in THF (10 mL) was added in dropwise in 10 minutes. After stirring for an additional 10 minutes at -78°C, the solution was quenched with ethyl acetate and saturated sodium chloride solution. The organic phase was washed with saturated sodium bisulfite, saturated sodium chloride, dried with sodium sulfate and concentrated *in vacuo*. The residue was purified by flash chromatography (10% ethyl acetate in hexane) to yield the 0.23 g (90%) of the product of step 2: LC/MS (m/z 235, $(M+H)^+$); ^1H NMR ($CDCl_3$) δ 8.82 (d, 1H), 8.03 (dd, 1H), 7.90 (d, 1H), 7.44 (t, 1H), 7.26 (dd, 1H), 7.16 (s, 1H), 4.80 (s, 2H), 3.95 (s, 3H).

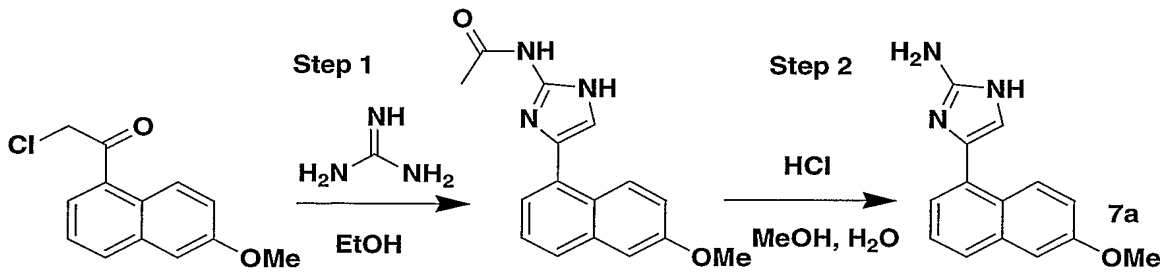
Step 3

To a solution of the product of step 2 (0.23 g, 1.0 mm0l, 1.0 equi.) in ethanol (5mL) at room temperature was added thiourea (90 mg, 1.2 mmol, 1.2 equi.). The reaction solution was stirred at room temperature for 2 hours, after which a yellow precipitate was formed. The reaction was quenched by addition of water and ethyl

acetate. The aqueous phase was extracted with ethyl acetate (3x). The combined organic phases were dried with sodium sulfate and concentrated *in vacuo* to yield 200 mg (78%) of the title compound **6a**: LC/MS (m/z 235, $(M+H)^+$); ^1H NMR ($CDCl_3$) δ 8.1 (d, 1H), 7.9 (m, 1H), 7.43 (m, 2H), 7.25 (m, 1H), 7.10 (dd, 1H), 6.65 (s, 1H), 3.95 (s, 3H).

Preparation 7

4-[1-(6-Methoxy)naphthyl]-3-aminoimidazole 7a



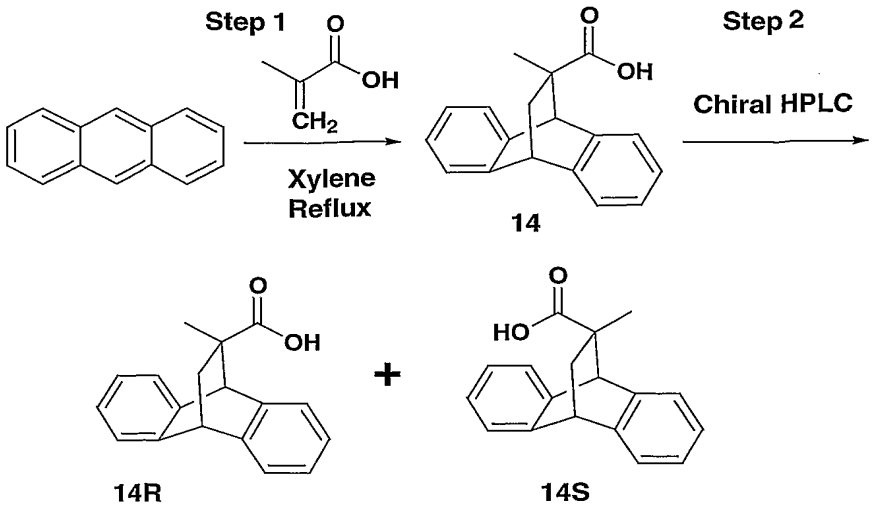
Step 1

To a solution of the product of preparation 6, step 2 (0.5 g, 2.14 mmol, 1.0 equi.), in ethanol (5 mL) at room temperature was added 1-acetylguanidine (650 mg, 6.42 mmol, 3.0 equi.). The reaction solution was stirred at room temperature for 24 hours. The reaction was quenched by addition of water and ethyl acetate. The aqueous phase was extracted with ethyl acetate (3x). The combined organic phases were dried with sodium sulfate and concentrated *in vacuo* to yield 0.2 g (35%) of the product of step 1: LC/MS (m/z 282, $(M+H)^+$).

Step 2

To a solution of the product of step 1 (0.2 g, 0.7 mmol, 1.0 equi.) in methanol (5 mL) was added water (1.0 mL) and hydrochloric acid (12N, 1.0 mL). The reaction solution was heated to reflux for 1 hour, after which the solvent was removed *in vacuo*. The crude mixture was purified by cation exchange SPE to give 0.12 g (70%) of the title compound **7a**: LC/MS (m/z 240, $(M+H)^+$).

Preparation 14



Step 1 Ref: B. Bacle and G. Levesque, *Polymer Communications*, 28, 36 (1987).

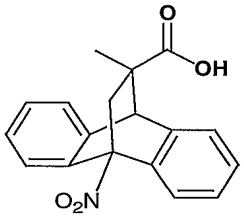
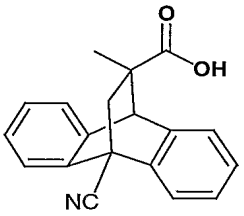
A 1L flask was charged with anthracene (14g, 0.078 mol, 1.0 equi.), hydroquinone (0.8g, 0.008 mol, 0.1 equi.), methacrylic acid (14 mL, 0.156 mol, 2.0 equi.) and xylene (500 mL). The solution was heated to reflux for 1 day. The solution was cooled and concentrated *in vacuo*. The residue was dissolved in ethyl acetate and extracted with 1N NaOH (3x). The aqueous phase was acidified with 1N HCl, and the product was extracted with ethyl acetate (3x). The combined organic phases were concentrated *in vacuo* to give the crude product mixture. Recrystallization with hexane and ethyl acetate to yield 8g (40%) of step 1, 14 :LC/MS (m/z 263 $(M-H)^+$); ^1H NMR ($CDCl_3$) δ 7.08-7.25 (m, 8H), 4.37 (s, 1H), 4.25(t, 1H), 2.61 (dd, 1H), 1.39 (dd, 1H), 1.07 (s, 3H).

Step 2

The product of step 1, 14 was resolved into its corresponding enantiomers, 14(R) and 14(S) by chiral preparative HPLC with the following conditions, Column: Chiracel®-OJ, 5 X 50 cm, Mobile phase: trifluroacetic acid/acetonitrile: 1/1000 (vol/vol), Temperature: ambient, Flowrate: 70 mL/min, Injection: 1.5 grams in 50 mL solvent, Detection: UV (250 nm). Retention times for R-enantiomer , 30 min, S-enantiomer, 52 min. Analytical HPLC conditions, Column: Chiracel®-OJ, 4.6 X 250 cm, Mobile phase: trifluroacetic acid/acetonitrile: 1/1000 (vol/vol), Temperature:

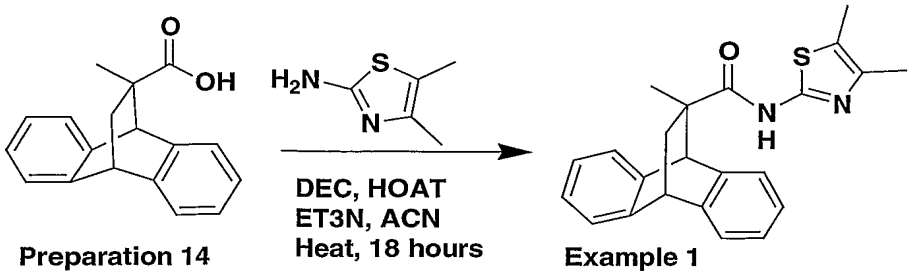
ambient, Flowrate: 1.5 mL/min, Detection: UV (250 nm). Retention times: R-enantiomer, 6.5 min, S-enantiomer, 15 min.

In a similar manner the following compounds were prepared from the corresponding 9-nitroanthracene and 9-anthracenecarbonitrile (Reference: P.V. Alston, R.M. Ottenbrite, J. Newby, J. Org. Chem. *J. Org. Chem. 44*, 4939 (1979)) and were resolved to the enantiomers according to the procedure of Step 2.

Preparation 14	Structure
14b	
14c	

Examples

Example 1 (compound 1)

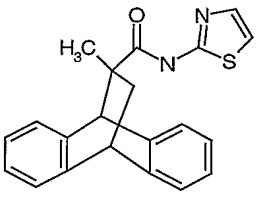
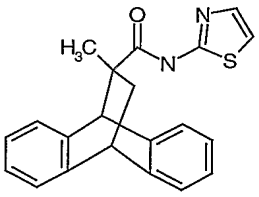
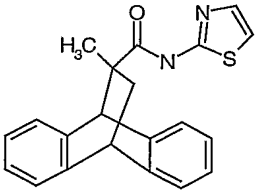


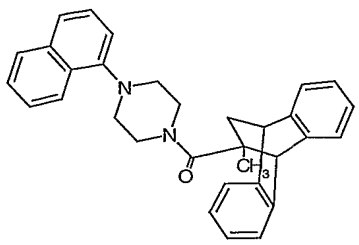
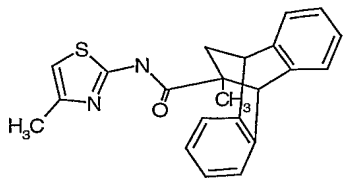
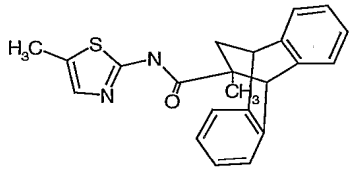
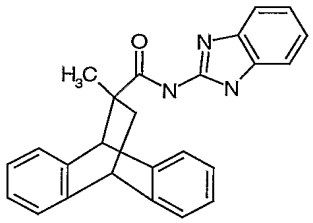
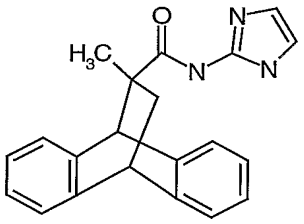
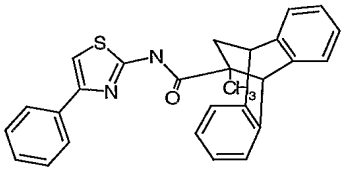
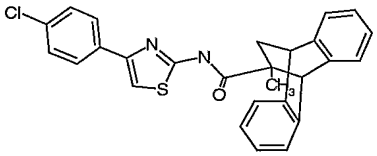
Preparation 14 Example 1

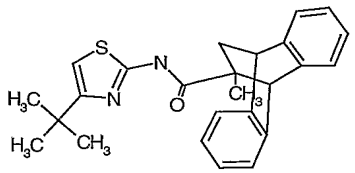
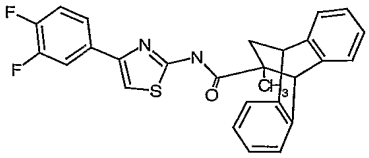
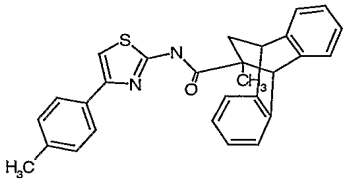
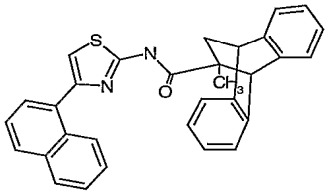
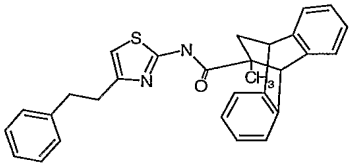
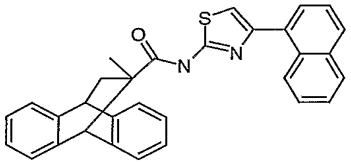
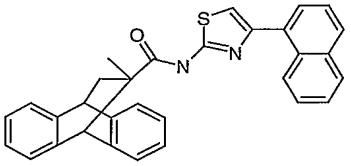
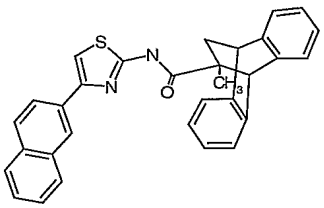
To a solution of the product of Preparation 14, step 1 (20 mg, 0.075 mmol, 1.0 equi.) in acetonitrile (2 mL) was added 1-[3-(dimethylamino) propyl]-3-

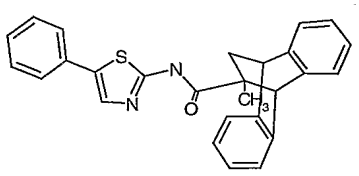
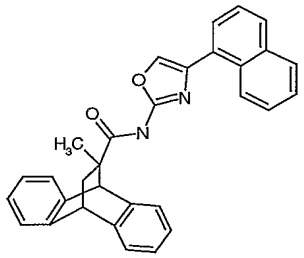
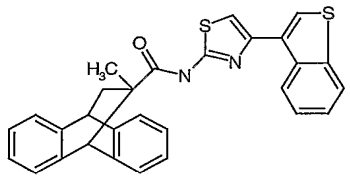
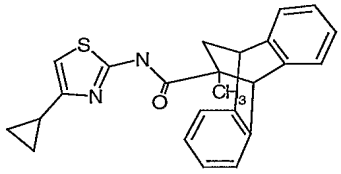
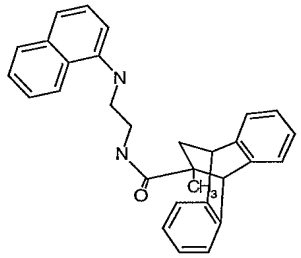
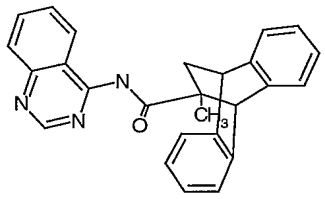
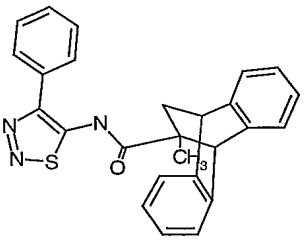
ethylcarbodiimide hydrochloride (DEC) (17 mg, 0.09 mmol, 1.2 equi.), 1-hydroxy-7-azabenzotriazole (HOAt) (12 mg. 0.09 mmol, 1.2 equi.), triethyl amine (0.025 mL, 0.18 mmol, 2.5 equi.), and 2-amino-4,5-dimethylthiazole hydrochloride salt (14.8 mg, 0.09 mmol, 1.2 equi.). The reaction solution was heated to 80°C for 18 hours. The reaction was then concentrated *in vacuo*. The product mixture was purified by flash chromatography (20% ethyl acetate in hexane) to yield 19.8 mg (70%) of Example 1. LC/MS (m/z 375, (M+H)+.

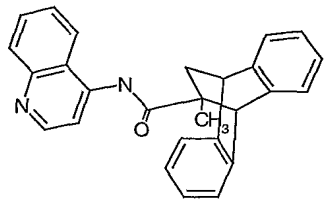
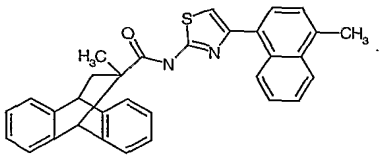
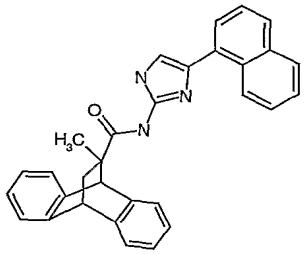
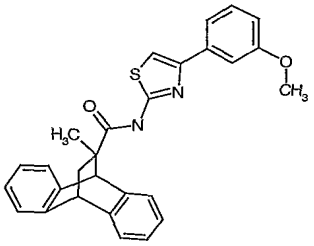
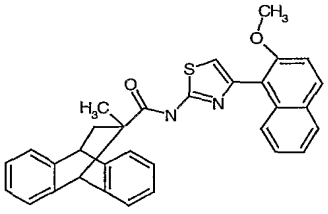
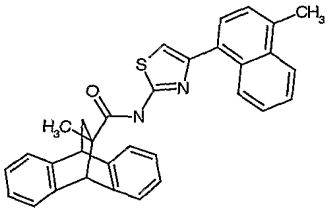
In a similar manner Examples **2-51** were prepared from the coupling of the appropriate acids (14, 14R, 14S, 14a, 14aR, 14aS, 14b, 14bR, 14bS)) prepared as described in Preparation 14 and the appropriate amines. Preparations of amines not commercially available are described in the preceding preparations section of this document. All examples in the tables are racemic unless specified otherwise. Examples in the table where one enantiomer predominates or is the sole component, are designated as either R or S.

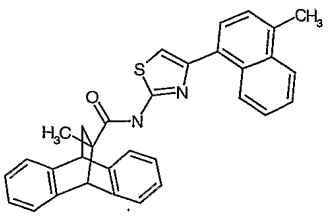
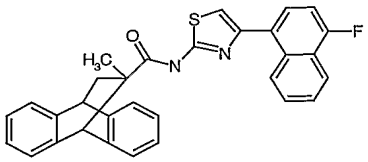
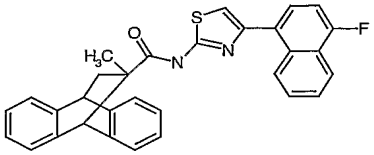
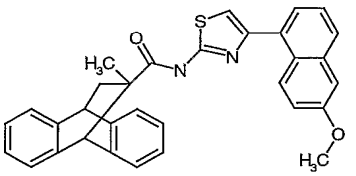
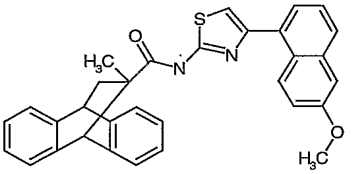
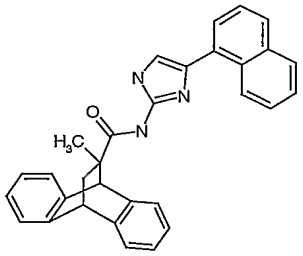
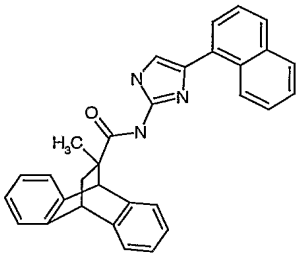
Example Number	**Compound Number**	**Chiral Compounds**	**Structure**	**MS: (M+H = MW shown +1)**
2	2			
3	3	**Chiral (R)**		
4	4	**Chiral (S)**		

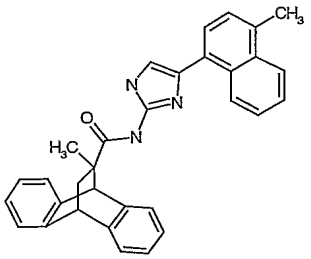
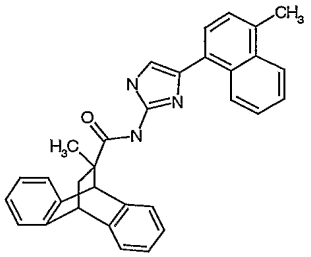
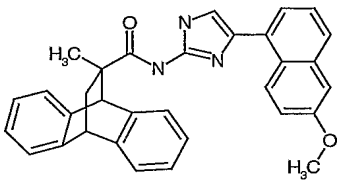
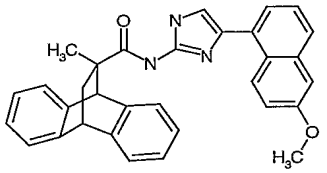
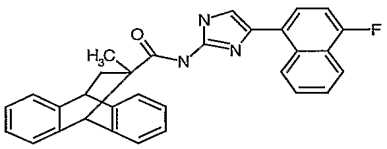
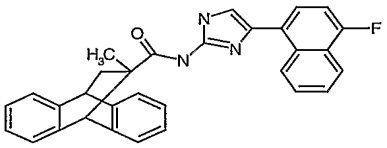
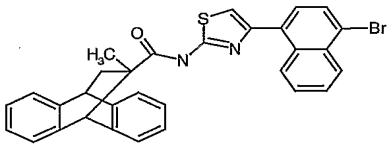
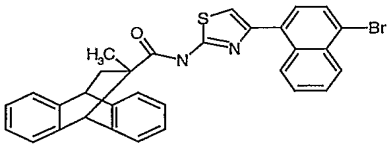
5	5		
6	6		360.5
7	7		360.5
8	8		379.47
9	9		329.41
10	10		422.6
11	11		457

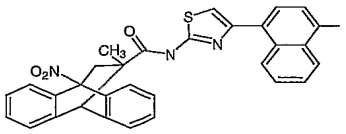
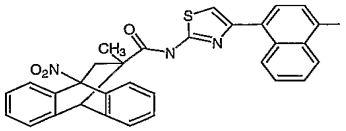
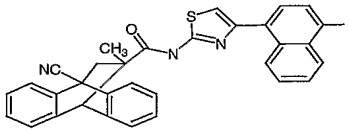
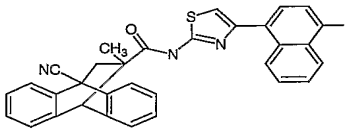
12	12			402.6
13	13			458.5
14	14			436.6
15	15			472.6
16	16			450.6
17	17	**Chiral (R)**		472.61
18	18	**Chiral (S)**		472.61
19	19			472.6

20	20		422.55
21	21		456.55
22	22		478.64
23	23		386.5
24	24		432.57
25	25		391.5
26	26		423.5

27	27			390.5
28	28			486.64
29	29			455.56
30	30			452.58
31	31			502.64
32	32	**Chiral (R)**		486.64

33	33	**Chiral (S)**		486.64
34	34	**Chiral (R)**		490.6
35	35	**Chiral (S)**		490.6
36	36	**Chiral (S)**		502.64
37	37	**Chiral (R)**		502.64
38	38	**Chiral (S)**		455.56
39	39	**Chiral (R)**		455.56

40	40	**Chiral (S)**		469.59
41	41	**Chiral (R)**		469.59
42	42	**Chiral (S)**		485.59
43	43	**Chiral (R)**		485.59
44	44	**Chiral (S)**		473.55
45	45	**Chiral (R)**		473.55
46	46	**Chiral (R)**		551.51
47	47	**Chiral (S)**		551.51

48	48	**Chiral (R)**		532.29
49	49	**Chiral (S)**		532.29
50	50	**Chiral (R)**		512.27
51	51	**Chiral (S)**		512.24

Example 2

Site I Binding Assay

In order to measure the binding of compounds to Site I on the glucocorticoid receptor a commercially available kit was used (Glucocorticoid receptor competitor assay kit, Panvera Co., Madison, WI). Briefly, a cell lysate containing recombinantly expressed human full-length glucocorticoid receptor was mixed with a fluorescently labeled glucocorticoid (4nM FITC-dexamethasone) plus or minus test molecule. After one hour at room temperature, the fluorescence polarization (FP) of the samples were measured. The FP of a mixture of receptor, fluorescent probe (i.e. FITC-dexamethasone) and 1mM dexamethasone represented background fluorescence or 100% inhibition, whereas, the FP of the mixture without dexamethasone was taken to be 100% binding. The percentage inhibition of test molecules were then compared to the sample with 1mM dexamethasone and expressed as % relative binding activity with dexamethasone being 100% and no inhibition is 0%. Test molecules were analyzed in the concentration range from 0.1nM to 40 μM.

Site I binding assays for any NHR are conducted similarly to the above. An appropriate cell lysate or purified NHR is used as the source of the NHR. The

fluorescent probe and unlabeled competitor are appropriate for the specific NHR, i.e. are ligands for the specific NHR.

Example 3

Cellular Transrepressional Assay

To measure the ability of test molecules to inhibit AP-1 induced transcriptional activity we utilized an A549 cell which was stably transfected with a plasmid containing 7x AP-1 DNA binding sites (pAP-1-Luc plasmid , Stratagene Co. La Jolla, CA) followed by the gene for luciferase. Cells were activated with 10ng/ml of phorbol myristic acid (PMA) plus or minus test molecules for 7 hours. After 7 hours a luciferase reagent was added to measure luciferase enzymatic activity in the cell. After a 10 minute incubation of luciferase reagent with cells, luminescence was measured in a TopCount luminescence counter. Repression of AP-1 activity was calculated as the percentage decrease in the signal induced by PMA alone. Test molecules were analyzed in the concentration range from 0.1nM to 40 μM. IC50s were determined by using standard curve fitting methods such as Excel fit (Microsoft Co.). An IC50 is the test molecule concentration which causes a 50% repression of transcription, i.e. a 50% reduction of AP-1 activity.

Other reporters and cell lines also may be used in a cellular transrepressional assay. A similar assay is performed in which NF-κB activity is measured. A plasmid containing NF-κB DNA binding sites is used, such as pNF-kB-Luc, (Stratagene, LaJolla CA), and PMA or another stimulus, such as TNF-α or lipopolysaccharide, is used to activate the NF-κB pathway. NF-κB assays similar to that described in Yamamoto K., et al., J Biol Chem 1995 Dec 29;270(52):31315-20 may be used.

The cellular transrepressional assays described above may be used to measure transrepression by any NHR. One of skill in the art will understand that assays may require the addition of components, such as a stimulus (eg. PMA, lipopolysaccharide, TNF-α, etc) which will induce transcription mediated by AP-1 or NF-κB. Additionally, AR mediated transrepression may be measured by the assay described in Palvimo JJ, et al. J Biol Chem 1996 Sep 27;271(39):24151-6, and PR mediated transrepression may be measured by the assay described in Kalkhoven E., et al. J Biol Chem 1996 Mar 15;271(11):6217-24.

Example 4

Cellular Transcriptional Assay

In order to measure the ability of compounds to induce DNA binding and transcriptional activation in cells the following assay was performed. A HeLa cell line was stably transfected with a gene expressing a fusion protein consisting of the GAL4 DNA binding domain linked to the ligand binding domain of GR. Also transfected into these cells was a DNA binding site for GAL4 (5 repetitions of a 17-mer GAL4 binding site) linked to the beta-globin reporter in front of the luciferase gene. See Eisenmann, G., Cheynel, and Gronemeyer, H. (1995), Quand les cellules scintillent, Biofutur (Le Technoscope), 151 : 8. Cells were incubated for 20 hours with either dexamethasone or test molecule. After 20 hours the level of luciferase activity was measured using a Steady Glo Luciferase assay system (Promega Co., Madison, WI). Induction of luciferase activity with 100nM dexamethasone was considered 100% activation. The activity of test molecules was measured as a percentage of dexamethasone induced DNA binding (transactivation). EC50s were calculated by using standard curve fitting methods such as Excel Fit (Microsoft Co., Redmond, WA). An EC50 is the test molecule concentration required to cause a 50% stimulation of transcription.

A second assay which measures the ability of compounds to induce the expression of tyrosine amino transferase mRNA in liver cells was also utilized to determine the ability of compounds to induce DNA binding. In these experiments, an HTC cell line was treated with dexamethasone or test molecules for 20 hours followed by mRNA extraction and analysis by RT-PCR. Again, dexamethasone induction (100 nM) was considered 100% activation. Test molecules were analyzed in the concentration range from 0.1 nM to 40 μM.

Cellular transcription transactivated by any NHR may be measured using an assay similar to the one described above for GR. That is, the NHR (either full length or the ligand binding domain) of interest is overexpressed in a suitable cell line such as COS. A plasmid which contains the DNA binding element specific for the NHR attached to a promoter and linked upstream of a reporter gene (e.g. luciferase), is co-transfected with the NHR. A chimeric NHR- ligand binding domain fused to GAL4,

or other transcription factor, could also be used to measure transactivation mediated by ligand binding to the NHR. In this case, the DNA binding element would be specific for the NHR fusion partner. An appropriate nuclear hormone is used for comparison to the test molecule. The cell line is treated with test molecule and reporter gene activity measured.

Example 5

GR Binding Activity, AP-1 Inhibitory Activity, and Transactivational Activity of Racemic Mixtures

Each of the twenty-seven racemic mixtures described in Example 1 was tested in the GR Site I binding assay, the cellular transrepressional assay, and the cellular transcriptional assay. The results are given in Table II below, in Example 10. GR Site I binding of the compounds ranged from 20.0 – 99.1 % inhibition at 10 μM concentration. AP-1 inhibition in the cellular transrepressional assay ranged from 0.8 – 82.9 % at 10 μM concentration. EC50s for DNA binding in the cellular transcriptional were determined for some of the compounds and were greater than 40 μM for all but one.

The EC50 for dexamethasone induction of tyrosine amino transferase mRNA in the HTC cell line is approximately 50nM. Two racemic mixtures of Example 1 were analyzed in the tyrosine amino transferase mRNA assay and had EC50s of greater than 40 μM.

Example 6

Enantiomeric Separation of Twelve Racemates

Twelve compounds which were originally synthesized as racemic mixtures were separated into enantiomeric pairs, and the enantiomeric identity of each member of the pair was determined using standard techniques known in the art. These twenty-four enantiomers are among the compounds of Example 1.

Example 7

GR Binding Activity, AP-1 Inhibitory Activity, and Transactivational Activity of Twenty-four Enantiomers

Each of the twenty-four enantiomers was tested in the cellular transcriptional assay. All but one of the twenty-four enantiomers were tested in the cellular transrepressional assay. Most of the twenty-four enantiomers were tested in the GR Site I binding assay. Two enantiomers (one pair) were tested in the tyrosine amino transferase mRNA assay.

EC50s for DNA binding in the cellular transcriptional assay were greater than 40 μM for all but three of the twelve S enantiomers and for all but two of the twelve R enantiomers. For ten of the S enantiomers, EC50s for DNA binding in the cellular transcriptional assay were greater than 40 μM for all but one. For ten of the R enantiomers, EC50s for DNA binding in the cellular transcriptional assay were greater than 40 μM for all. IC50s for AP-1 inhibition in the cellular transrepressional assay ranged from 15 nM to 11 μM for the twelve S enantiomers, with the range for eleven of the S enantiomers being 15 nM to 275 nM. IC50s for AP-1 inhibition in the cellular transrepressional assay ranged from 33 nM to 11 μM for ten of the S enantiomers, with the range for nine of those S enatiomers being 33 nM to 275 nM. IC50s for AP-1 inhibition in the cellular transrepressional assay ranged from 222 nM to 40 μM for the twelve R enantiomers, with the range for ten of the R enantiomers being 650 nM to 40 μM. GR Site I binding inhibition at 10 μM ranged from 6.1% to 41% for the S enantiomers, and from 51.8% to 99% for the R enantiomers, with the range being 51.8% to 97.9% for ten of the R enantiomers. Both enantiomers of the pair tested had EC50s of greater than 40 μM in the tyrosine amino transferase mRNA assay.

This data clearly shows that the S enantiomers were more potent inhibitors of AP-1 activity relative to the R enantiomers. In contrast, the R enantiomers were more potent inhibitors of dexamethsone binding to GR compared to the S enantiomers.

Example 8

Dissociation of Twenty-four Enantiomers Compounds

The dissociation of the twenty-four enantiomers was calculated by dividing the EC50 from the cellular transcriptional assay by the IC50 from the cellular transrepressional assay. The dissociation constant for the R enantiomers ranged from 62.5 to 1.0. The dissociation value for the S enantiomers ranged from 1000 to 0.91,

with the dissociation value for eleven of the S enantiomers ranging from 1000 to 137, and the dissociation value for some of the S enantiomers ranging from 1000 to 167.

Example 9

GR Homology Model

The GR homology model of the ligand binding domain (LBD) was constructed using known methodology. Specifically, the human sequence (QRHUGA obtained from the International Protein Sequence Database, pir.georgetown.edu/pirwww), residues 523-777 (SEQ ID NO:1), comprising the LBD was aligned to the human PR sequence (LBD residues 682-932) (SEQ ID NO:2) available as a xray-structure (1A28.pdb obtained from the RCSB, the Research Collaboratory for Structural Bioinformatics, www.rcsb.org/pdb) using the modeler module within InsightII (Version 2000, MSI/Accelrys).

```
  GR: 523 ATLPQLTPTLVSLLEVIEPEVLYAGYDSSVPDSTWRIMTTLNMLGGRQVI 572
1A28: 682     QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLL 727

  GR: 573 AAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQSSANLLC 622
1A28: 728 SVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLY 777

  GR: 623 FAPDLIINEQRMTLPCMYDQCKHMLYVSSELHRLQVSYEEYLCMKTLLLL 672
1A28: 778 FAPDLILNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLL 827

  GR: 673 SSVPKDGLKSQELFDEIRMTYIKELGKAIVKRE-GN-SSQNWQRFYQLTK 720
1A28: 828 NTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSS--QRFYQLTK 875

  GR: 721 LLDSMHEVVENLLNYCFQTFLDKTM-SIEFPEMLAEIITNQIPKYSNGNI 769
1A28: 876 LLDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMV 925

  GR: 770 KKLLFHQK 777
1A28: 926 KPLLFH-K 932
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The resulting GR LBD homology model coordinates are provided in Table I, which for convenience is located at the end of this specification under the heading Example 21.

Example 10

Identification of Site II

The classical ligand binding site, i.e. Site I, is defined by the immediate space surrounding progesterone in 1A28.pdb, can be further defined by the amino acid residues in contact with progesterone, and are well known in the art. The analogous GR site I residues were identified as those proximate to a modeled version of dexamethasone in the GR homology model. GR Site I residues in contact with dexamethasone (as found in the GR homology model) are M560, L563, N564, L566, G567, Q570, M601, M604, A605, L608, R611, F623, M639, Q642, M646, L732, Y735, C736, T739 and E748. The present invention is based on the discovery of an alternate binding site, herein known as Site II, present in a number of NHRs (nuclear hormone receptors), in particular in GR, which interacts with small molecule modulators. In the case of GR, a ligand binding to Site II results in a transrepression signaling within cells (inhibition of AP-1 or NF-κB). The location of Site II is defined herein for a number of related NHRs and specifically for GR in Figure 2. GR Site II residues include the following (using GR numbering): E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667.

The identification of Site II is supported by the three-dimensional complementarity of shape and functional features between the site and ligands having in vivo transrepression activity. An example of such complementarity is shown in Figure 3, wherein the S-enantiomer of Compound 15 was manually docked into the GR homology model of Site II.

Site I and Site II residues were defined as those capable of van der Waal's contact with a ligand contained by those residues. Using dexamethasone for Site I (bound in a similar manner as that reported for progesterone in PR Site I) and Compound 15 for Site II (manually docked as shown in Figure 3), all residues capable of vander Waal's contact were listed as site residues. Included as well were those residues not in immediate contact with either ligand, but capable of such contact if the space between ligand and residue was occupied by a small molecule fragment.

In addition, computations of binding energetics for a series of twenty-seven related Site II ligands, which are among the compounds described in Example 1, was

found to correlate with the observed in vivo transrepression activities, providing further evidence of the critical role of Site II binding in producing an in vivo transrepression effect. Correlation data are shown in Table II (below) and Figure 5, and structures are shown in Figure 4. Although the data reflect the activities of racemates, each individual molecule was modeled as the S-enantiomer for purposes of consistency. These twenty-seven compounds showed % inhibition at 10 μM in the cellular tranrepressional assay ranging from 0.8 to 82.9. The EC50 in the cellular transcriptional assay was greater than 40 μM for twenty-six of the compounds, and was greater than 10 μM for the remaining compound.

Binding energetics were calculated using Flo (Colin McMartin, Thistlesoft, High Meadow, 603 Colebrook Road, Colebrook, CT 06021), molecular modeling software which utilizes the Amber molecular mechanics force field to achieve a best fit between ligand and protein binding site. Both the ligand and Site II residues in contact with the ligand are allowed to undergo energy minimization and geometry optimization. The result of these operations provides an optimum ligand binding orientation and a series of calculated energies of interaction. The correlation between observed AP-1 inhibition (percent at 10 uM) and binding energetics is based on the calculated non-bonded contact interactions between ligand and protein residues. This type of calculation generally reflects the degree to which a ligand conforms to the shape of the binding site.

Table II, below, gives correlation data calculated for the analogues of Compound 15 using Flo Contact Energy Scores (Ecnt) after manually docking each analogue into GR Site II (Flo modeling software, Colin McMartin, ThistleSoft). %AP-1 values were determined at an inhibitor concentration of 10 μM. GR binding assay was performed as described in Example 2. DNA binding assay was performed as described in Example 4. AP-1 inhibition assay was performed as described in Example 3.

Table II

Compound	GR Binding (% @ 10 uM)	DNA Binding NP-1 IC50 (uM)	AP-1 (%inh @ 10 uM)	Ecnt (KJ/mol)
	92.1		30.3	-18.7
	99.1		24.5	-15.6
	97.6		0.8	-17
	85.1	> 10	29.5	-16.9
	92.8	>40	8.7	-15.1
	96.0		36.1	-22.5
	91.0		15.2	-19.2
	84.9	>40	58.6	-19.4
	92.3		25.1	-13.3
	93.2		41.3	-22.9
	88.1	>40	61.8	-28.9
	88.3		22.5	-20.2
	92.2		29.3	-15.2
	93.5		33.6	-18.4
	65.7		61.8	-26.3
	93.8		26.4	-27.6
	94.1		23.4	-16.3
	94.4		47	-18.9
	76.8		7	-21.9
	20.0		13.6	-27.8
	64.5		32.7	-18.9
	45.3		8.6	-23.3
	31.9		18.9	-21.5
	90.4	>40	82.9	-29.6
	56.3	>40	64.2	-21.2
	88.7		38.5	-23.7
	91.7		43.8	-25

There are a number of published examples wherein the energetics of interaction of docked structures correlated with observed activity; one such example was in the use of AutoDock (Sybyl, Tripos, St. Louis, MO) in evaluating 27 HIV-1 Protease inhibitors (Huang, et. al., J. Med. Chem. 45, 333, 2002). Energies of interaction between the HIV-1 protease active site and a series of ligands were calculated using an MM2X force field and found to correlate with observed activities (Holloway and Wai in Computer-Aided Molecular Design, ACS Symposium Series 589, ACS, Washington, DC 1995). The solvation contribution to the binding energetics of docked structures was accounted for and provided the means to more accurately predict biological activities (Takamatsu and Itai, Proteins: Structure, Function, and Genetics, 33:62-73, 1998).

Correlating structure with activity is a fundamental criterion in pointing out those aspects of the structure most relevant to activity. When the correlation is carried out with ligands alone, it can demonstrate which properties/features of the ligands are important for activity. When done with a protein binding site acting as a constraint, the correlation provides evidence that certain three-dimensional binding site features are important. Thus, when a correlation exists between AP-1 inhibition data and the calculated binding energetics for a series of molecules, this provides a reasonable certainty that the binding site model is consistent with the observed inhibition data. Therefore, the design of molecules having features complementary to those of the binding site should lead to the effective structure-based design of novel ligands having desired biological activity, in this case, AP-1 inhibition.

A recent publication (Bledsoe, et. al., Cell, online publication by Cell Press, July 1, 2002; DOI: 10.1016/S0092867402008176) describes the successful crystallization and xray structural elucidation of the glucocorticoid receptor LBD as the dimer. Disruption of the dimeric structure was found to occur upon mutation of selected residues at the dimerization interface. These mutants lacked transactivation activity and retained transrepression activity. Interestingly, the dimerization interface and the opening of Site II share the same outer surface (two residues located at the rim of Site II, namely, Q615 and P625, are among several identified by the authors as critical to dimer formation). This observation is consistent with the proposed importance of Site II in modulating dissociated steroid activity.

Example 11

Cellular Transrepressional Assay with Both A Site II Dissociated Compound and Dexamethasone

The cellular transrepressional assay was performed by determining the IC50 for transrepression for dexamethasone in the presence or absence of one of the compounds (an S enantiomer) of Example 1. This S enantiomer is hereinafter referred to as Compound A. In the absence of Compound A dexamethasone yielded an IC50 of 3.4 nM with a maximum percent inhibition of 75%, whereas, in the presence of 800nM of the compound the IC50 decreased to 1.2 nM with 100% inhibition. This showed that there is an additive effect of adding the compound with dexamethasone.

Example 12

Cellular Transcriptional Assay with Both A Site II Dissociated Compound and Dexamethasone

For transactivation, the compound used in Example 11, Compound A, was an antagonist of dexamethasone activity. Here, an EC50 was determined in the cellular transcriptional assay for dexamethasone in the presence or absence of the compound. In the absence, the EC50 was 3.4nM with 100% stimulation, whereas, in the presence of the compound the EC50 shifted to 8.5nM with 47% stimulation.

Example 13

Overlay of Site II from Various NHRs and Calculation of rms

Consensus alignments were carried out using ICM (Molsoft LLC, La Jolla, CA) between human GR LBD and other human NHR LBDs. Figure 2 shows the alignment, indicating by shading the residues of Site II in each NHR, i.e. residues corresponding to residues of GR Site II. Dots are spaceholders and do not represent amino acids. Numbers refer to the first residue in each line, are specific for each NHR and are based on the full-length NHR. For the NHRs listed below, with the exception of GR and MR, structural data was obtained from the RCSB references listed below, and the numbering system in the RCSB references was used. For GR

and MR, structural data was obtained by homology modeling using the literature references below, and the numbering system in those literature references was used. The RCSB references (in parentheses) and literature references for the various NHRs are as follows:

RXRalpha (1lbd) Bourguet, W., Ruff, M., Chambon, P., Gronemeyer, H., Moras, D. Nature 375 pp. 377 (1995); PPAR-gamma (2prg) Nolte, R. T., Wisely, G. B., Westin, S., Cobb, J. E., Lambert, M. H., Kurokawa, R., Rosenfeld, M. G., Willson, T. M., Glass, C. K., Milburn, M. V. Nature 395 pp. 137 (1998); RARgamma (2lbd) Renaud, J. P., Rochel, N., Ruff, M., Vivat, V., Chambon, P., Gronemeyer, H., Moras, D. Nature 378 pp. 681 (1995); PR (1a28) Williams, S. P., Sigler, P. B. Nature 393 pp. 392 (1998); VitDR (1db1) Rochel, N., Wurtz, J. M., Mitschler, A., Klaholz, B., Moras, D. Mol. Cell 5 pp. 173 (2000); AR (1e3g) Matias, P. M., Donner, P., Coelho, R., Thomaz, M., Peixoto, C., Macedo, S., Otto, N., Joschko, S., Scholz, P., Wegg, A., Basler, S., Schafer, M., Egner, U., Carrondo, M. A. J.Biol.Chem. 275 pp. 26164 (2000); ERalpha (1a52) Tanenbaum, D. M., Wang, Y., Williams, S. P., Sigler, P. B. Proc Natl Acad Sci U S A 95 pp. 5998 (1998); ERbeta (1l2j) Shiau, A. K., Barstad, D., Radek, J. T., Meyers, M. J., Nettles, K. W., Katzenellenbogen, B. S., Katzenellenbogen, J. A., Agard, D. A., Greene, G. L. Nat.Struct.Biol. 9 pp. 359 (2002); TRbeta (1bsx) Wagner, R. L., Darimont, B. D., Apriletti, J. W., Stallcup, M. R., Kushner, P. J., Baxter, J. D., Fletterick, R. J., Yamamoto, K. R. Genes Dev. 12 pp. 3343 (1998). MR and GR structural data were obtained by homology modeling to PR using the sequences from the following references: GR, PIR Accession Number QRHUGA, Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G.,Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M., Nature (1985) 318: 635-641; MR, PIR Accession Number A29613, Arriza, J.L.; Weinberger, C., Cerelli, G., Glaser, T.M., Handelin, B.L., Housman, D.E., Evans, R.M., Science (1987) 237: 268-275.

It is understood that Figure 2 is merely illustrative of the invention and is not intended to be limiting in any manner. Accordingly, it is understood that corresponding amino acid residues of other nuclear receptors such as other estrogen receptors, thyroid receptors, retinoid receptors, glucocorticoid receptors, progestin

receptors, mineralocorticoid receptors, androgen receptors, peroxisome receptors and vitamin D receptors may also be used in the methods of the invention.

The structure coordinates of Site II in the NHRs of Figure 2 are given in Table III, located under the heading for Example 22.

Using structural data described above for several NHR LBDs, rigid fitting operations were conducted between the GR LBD homology model and the following closely-related NHRs: progesterone receptor LBD, androgen receptor LBD, estrogen receptor alpha LBD and estrogen receptor beta LBD. The fitting operation yielded Site II rms deviations in backbone atom comparisons of 0.57-0.71 Å. The fitting operations were carried out using the Match option within InsightII. Backbone atoms of GR Site II were compared to those of the following four NHRs: progesterone receptor (rms = 0.57 Å), androgen receptor (rms = 0.71 Å), estrogen receptor alpha (rms = 0.69 Å), and estrogen receptor beta (rms = 0.52 Å).

Example 14

Sequence Alignment of GR Site II from Various Species

Sequence alignments were prepared of the human GR and the GR from various non-human species. The sequence alignments were conducted using the program LOOK (Version 3.5.2 Molecular Applications Group, Palo Alto, CA). The alignment is shown in Figure 6. The sequence for each GR starts at residue 1. Alignments were made based on pair-wise sequence identity. Site II residues are shaded. GR sequences were obtained from the following sources: Squirrel (Saimiri boliviensis boliviensis) (GenBank U87951) Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); Pig GR (GenBank AF141371) Gutscher,M., Eder,S., Mueller,M. and Claus,R. Submitted to GenBank (08-APR-1999) Institut fuer Tierhaltung und Tierzuechtung (470), FG Tierhaltung und Leistungsphysiologie, Universitaet Hohenheim, Garbenstr. 17, Stuttgart 70599, Germany; Guinea Pig (GenBank L13196) Keightley,M.C. and Fuller,P.J. Mol. Endocrinol. 8 (4), 431-439 (1994); Marmoset (GenBank U87953) Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); Ma'z Monkey (GenBank U87952) Reynolds,P.D., Pittler,S.J. and Scammell,J.G. J. Clin. Endocrinol. Metab. 82 (2), 465-472 (1997); rat (GenBank M14053)

Miesfeld,R., Rusconi,S., Godowski,P.J., Maler,B.A., Okret,S., Wikstrom,A.C., Gustafsson,J.A. and Yamamoto,K.R. Cell 46 (3), 389-399 (1986); mouse (GenBank X04435) Danielsen,M., Northrop,J.P. and Ringold,G.M. EMBO J. 5 (10), 2513-2522 (1986); Human (Protein Information Resource QRHUGA) Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G., Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M., Nature (1985) 318: 635-641.

Example 15

Site II Binding Assay

In order to measure binding of a test molecule (i.e. a potential ligand) to Site II on GR, a labeled, such as radiolabeled or fluorescently labeled, known ligand of Site II is prepared. Several approaches can be utilized to identify a ligand of Site II that can be used as the labeled known ligand of Site II. All involve analyzing a modulator of GR to determine if it is a ligand of Site II. Three such approaches follow.

The first approach involves making mutations in GR in site II. These Site II mutants are expressed in the transactivation and/or transrepression assays to determine if there is any alteration of the modulator's activity. It would be predicted that those amino acids which are in proximity to the compound, if mutated, should decrease the activity of the modulator in the transrepression assay, whereas, there should be no effect on the activity of dexamethsone mediated tranactivation and/or transrepression. This approach is used in Example 16.

A second approach is to prepare a modulator with a moiety that can be crosslinked to GR, such as dexamethasone mesylate. After crosslinking, the GR is digested with proteases and analyzed by mass spectrometry. The peptide(s) with a covalently attached modulator are identified.

A third approach is to crystallize the GR with the modulator. The structure of the co-crystal complex definitively shows the mode in which the modulator is binding to GR.

Once a ligand is identified, it is labeled and is used in the assay to measure binding of a test molecule to Site II. The test molecule and the labeled ligand are incubated with a cell lysate or purified complex containing GR. The binding of compounds to GR are measured using techniques which are standard in the art such as

fluorescence quenching, fluorescence polarization, filter binding, scintillation proximity assay, among others. The readout, such as fluorescence polarization, of a mixture of receptor, labeled ligand and 1mM unlabeled ligand represents 100% competition, whereas, the readout of the mixture without unlabeled ligand is taken to be 100% binding. The percentage competition of test molecules are then compared to the sample with 1mM unlabeled ligand and expressed as % relative binding activity with unlabeled ligand being 100% and no competition being 0%. Test molecules are analyzed in the concentration range from 0.1nM to 40 μM.

To confirm binding of a test molecule to Site II, a GR that has mutations in Site II may be used. It would be expected that a GR with mutations in Site II would have a diminished ability to be modulated by a ligand of Site II. Modulation by the test molecule, i.e. transrepression and transactivation, is compared between the native GR and the mutant GR.

Site II binding may also be confirmed by demonstrating that a steroid known to bind to Site I, such as dexamethasone, does not compete for the binding of the test molecule to Site II.

To determine an IC50, a fixed concentration of labeled ligand is used and a titration with unlabeled test molecule is performed. Test molecules are analyzed in the concentration range from 0.1 nM to 40 μM.

A Site II binding assay may be prepared using any NHR in place of GR as described above. Cross-linking agents and ligands appropriate for the specific NHR are used.

Example 16

Transactivation Studies on GR Site-Directed Mutants

Several mutations in Site II of the human glucocorticoid receptor were made. Two mutations of Alanine 607 to either a valine or phenylalanine were made which were predicted to block the entrance of Site II ligands into the Site II pocket. Valine 543, which is on the interior of the Site II pocket, was mutated to phenylalanine, and this mutation was predicted to disrupt binding of compounds to Site II. A double mutant A607V/V543L was also made. These mutations were made using a

commercially available kit, Stratagene Quick Change XL Site Directed Mutagenesis Kit (Stratagene, La Jolla, CA).

COS cells were transfected with expression vectors for either the wild type or the various mutants. Cells were also transfected with a highly sensitive, artificial reporter consisting of two glucocorticoid response elements upstream of the gene for luciferase, the GRE2LUC reporter. (PROMEGA steady glo luciferase assay system, Promega, Madison, WI). After 24 hours the cells were then treated for an additional 24 hours with either dexamethasone (Dex), or Site II ligands. At the end of the incubation period, luciferase levels were measured using the PROMEGA steady glo luciferase assay system (Promega, Madison, WI).

The data is shown in Figure 8, in which RLU means relative light units. Figure 8 shows that in the wild type GR, both dexamethasone and Compound A can induce transactivation via the GRE2LUC reporter. However, in the A607F, A607V and V543F mutants, whereas dexamethsone induced transactivation of the reporter, Compound A did not. Compound A is indicated by the left, darker, solid bar in each pair of bars. Dexamethasone is indicated by the right, lighter, hatched bar in each pair of bars. The control is cells transfected with DNA vector alone (no GR) plus the GRE2LUC reporter. These data suggest that either Compound A interacts with amino acids V543 and A607 in Site II or the mutations prevent the interaction of Compound A with GR.

Glucocorticoid receptor transactivation activity is very sensitive to mutations which may alter the conformation of the receptor. As seen in Figure 8, some point mutations enhance the ability of dexamethasone to induce transactivation. This may occur due to, among other explanations, an increase in the ability of dexamethasone to bind to GR or increased ability to recruit co-activators. The double mutant caused a decrease in the ability of dexamethasone to induce transactivation perhaps due to a more dramatic effect on the conformation of GR and a decreased ability to bind to dexamethasone or recruit co-activators.

Example 17

Effect of Combining BMS Site II Compounds with Dexamethasone or RU486 on AP-1 MediatedTranscription

A549 cells stably transfected with an AP-1 reporter with a luciferase readout, as described in Example 3, were treated with various concentrations of compounds. As shown in Figure 9, a titration of dexamethasone was performed in the presence or absence of Compound A (an S enantiomer) or Compound B (the R enantiomer of Compound A). As seen in Figure 9, these compounds increase the percentage of inhibition of AP-1 relative to dexamethasone alone, suggesting there is an additive effect between these Site II compounds and dexamethasone. In contrast, RU486 (Hofmann TG, Hehner SP, Bacher S, Droge W, Schmitz ML. FEBS Lett. 1998 Dec 28;441(3):441-6), which is an antagonist of Site I, which is the dexamethasone binding site, inhibits the ability of dexamethasone to repress AP-1 activity. The data taken together demonstrates that Compound A and Compound B act in an additive fashion with compounds which interact with Site I, suggesting they act at an alternative Site II.

Example 18

An Assay to Indirectly Measure the Interaction of Site II Ligands with GR

In order to measure the binding of putative Site II compounds to GR we utilized the Glucocorticoid receptor competitor assay kit (Panvera Co., Madison, WI) in a modified version of the FITC-dexamethasone fluorescence polarization assay described in Example 2. In this assay, Compound D was added at a concentration of 200 nM, which yields approximately 50% inhibition of FITC-dexamethasone binding. Compound D (an R enantiomer) is Compound 50 of Example 1. Compound D is a ligand of Site II that inhibits via Site II FITC-dexamethasone binding to GR. To the mixture of cell lysate containing the glucocorticoid receptor, Compound D, and FITC-dexamethasone, various competitor Site II ligands which do not inhibit dexamethasone binding were added and the change in FITC-dexamethasone binding was measured. These competitor Site II ligands, all compounds of Example 1 and all S enantiomers, were: Compound A; Compound C, which is the S enantiomer of Compound D; and Compound E, yet another S enantiomer of Example 1. If the

competitor compound binds to Site II and displaces Compound D, then FITC-dexamethasone should rebind to GR. As shown in Figure 10, the competitor compounds are effective at displacing Compound D and allowing FITC-dexamethasone to rebind to GR. This assay can therefore measure the relative binding of compounds to the Site II on GR.

Example 19

Site II ligands act in a GR dependent fashion to repress AP-1 driven transcription

In order to determine whether the Site II ligands act via GR, COS cells, which do not express GR, were transfected with an AP-1 luciferase reporter (pAP-1-Luc plasmid, Stratagene, La Jolla, CA) plus or minus an expression construct for full length human GR. AP-1 activity was measured via luciferase reporter activity as described in Example 3. When GR was not present, neither 1 micromolar dexamethasone nor 40 micromolar Compound A significantly inhibited AP-1 activity. However, when GR was transfected into the cell, both dexamethasone and Compound A suppressed AP-1 activity. These results are shown in Figures 11a and 11b, in which the Y axis is relative light units (RLU). These data show that both of these ligands act in a GR dependent fashion.

Example 20

Provision of GR Site II X-ray Structure Coordinates and Calculations of rms

The GR Site II x-ray structure coordinates were discerned from the disclosure in WO 03/015692 A2, February 27, 2003, Apolito, et. al. and are provided in Table IV under the heading for Example 23. Apolito discloses x-ray structure coordinates of GR LBD, but does not disclose the existence or identity of Site II.

The GR Site II x-ray structure coordinates were discerned from the disclosure in Kauppi et. al., in the Journal of Biological Chemistry Online, JBC Papers In Press as DOI:10.1074/jbc.M212711200, April 9, 2003, RCSB file: 1nhz.pdb (GR LBD bound to an antagonist, RU 486) and are provided in Table V under the heading for Example 24. Kauppi discloses x-ray structure coordinates of GR LBD, but does not disclose the existence or identity of Site II.

. The homology model GR Site II coordinates of Table I were compared to the Site II coordinates available from the disclosures in WO 03/015692 A2, February 27, 2003 Apolito, et. al. and those published by Kauppi et. al., in the Journal of Biological Chemistry Online, JBC Papers In Press as DOI:10.1074/jbc.M212711200, April 9, 2003, RCSB file: 1nhz.pdb (GR LBD bound to an antagonist, RU 486). When the backbone atoms of the homology model Site II residues, ie, E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I were compared, root mean square deviations (rmsds) of 0.92 and 1.02 Å were obtained between the homology model of Table I Site II residues and the Apolito Site II residues, and between the homology model of Table I Site II residues and the Kauppi Site II residues, respectively. In both instances the Site II residues were first overlaid using the structure overlay option within the ICM (Version 3.0.017, Molsoft. LLC) modeling software. Using the rmslig program within the Flo (Colin McMartin, Thistlesoft) molecular modeling program afforded backbone rmsd calculations. These observations underscore the similarity of the Site II homology model structure to actual crystal structures.

Example 21

Structure Coordinates of GR LBD, Table I

Below is Table I, which gives the three-dimensional structure coordinates of the GR LBD homology model. The format used is based on that commonly used in the RCSB (Research Collaboratory for Structural Bioinformatics, pdb file format), and the fields listed from left to right are defined as follows: record name, atom serial number, atom name, residue name, chain identifier, residue sequence number, orthogonal coordinate for x in Ångstroms, orthogonal cordinate for y in Ångstroms, orthogonal coordinate for z in Ångstroms, occupancy, and temperature factor.

Table I. GR Homology Model Coordinates

ATOM	1	N	ALA	A	523	29.896	-1.364	107.714	1.00	0.00
ATOM	5	CA	ALA	A	523	30.095	-0.736	106.398	1.00	0.00
ATOM	6	CB	ALA	A	523	31.574	-0.448	106.160	1.00	0.00
ATOM	7	C	ALA	A	523	29.565	-1.627	105.280	1.00	0.00

ATOM	8	O	ALA	A	523	29.626	-2.860	105.361	1.00	0.00
ATOM	9	N	THR	A	524	29.027	-0.987	104.257	1.00	0.00
ATOM	11	CA	THR	A	524	28.493	-1.717	103.105	1.00	0.00
ATOM	12	CB	THR	A	524	27.666	-0.754	102.257	1.00	0.00
ATOM	13	OG1	THR	A	524	27.383	-1.389	101.016	1.00	0.00
ATOM	14	CG2	THR	A	524	28.428	0.532	101.951	1.00	0.00
ATOM	15	C	THR	A	524	29.607	-2.329	102.263	1.00	0.00
ATOM	16	O	THR	A	524	30.663	-1.720	102.058	1.00	0.00
ATOM	17	N	LEU	A	525	29.370	-3.559	101.836	1.00	0.00
ATOM	19	CA	LEU	A	525	30.275	-4.243	100.909	1.00	0.00
ATOM	20	CB	LEU	A	525	29.686	-5.626	100.629	1.00	0.00
ATOM	21	CG	LEU	A	525	30.626	-6.524	99.829	1.00	0.00
ATOM	22	CD1	LEU	A	525	31.867	-6.870	100.645	1.00	0.00
ATOM	23	CD2	LEU	A	525	29.912	-7.799	99.399	1.00	0.00
ATOM	24	C	LEU	A	525	30.360	-3.442	99.612	1.00	0.00
ATOM	25	O	LEU	A	525	29.329	-3.065	99.040	1.00	0.00
ATOM	26	N	PRO	A	526	31.578	-3.090	99.231	1.00	0.00
ATOM	27	CA	PRO	A	526	31.804	-2.331	98.002	1.00	0.00
ATOM	28	CB	PRO	A	526	33.272	-2.040	97.977	1.00	0.00
ATOM	29	CG	PRO	A	526	33.936	-2.705	99.171	1.00	0.00
ATOM	30	CD	PRO	A	526	32.819	-3.379	99.951	1.00	0.00
ATOM	31	C	PRO	A	526	31.377	-3.118	96.771	1.00	0.00
ATOM	32	O	PRO	A	526	31.487	-4.348	96.713	1.00	0.00
ATOM	33	N	GLN	A	527	30.814	-2.387	95.828	1.00	0.00
ATOM	35	CA	GLN	A	527	30.403	-2.963	94.547	1.00	0.00
ATOM	36	CB	GLN	A	527	29.511	-1.931	93.859	1.00	0.00
ATOM	37	CG	GLN	A	527	28.265	-2.549	93.224	1.00	0.00
ATOM	38	CD	GLN	A	527	28.482	-2.831	91.742	1.00	0.00
ATOM	39	OE1	GLN	A	527	29.078	-3.849	91.362	1.00	0.00
ATOM	40	NE2	GLN	A	527	28.005	-1.911	90.924	1.00	0.00
ATOM	43	C	GLN	A	527	31.655	-3.268	93.726	1.00	0.00
ATOM	44	O	GLN	A	527	32.671	-2.574	93.856	1.00	0.00
ATOM	45	N	LEU	A	528	31.578	-4.294	92.894	1.00	0.00
ATOM	47	CA	LEU	A	528	32.746	-4.723	92.118	1.00	0.00
ATOM	48	CB	LEU	A	528	32.560	-6.180	91.716	1.00	0.00
ATOM	49	CG	LEU	A	528	32.452	-7.090	92.933	1.00	0.00
ATOM	50	CD1	LEU	A	528	32.112	-8.515	92.513	1.00	0.00
ATOM	51	CD2	LEU	A	528	33.737	-7.059	93.757	1.00	0.00
ATOM	52	C	LEU	A	528	32.898	-3.866	90.870	1.00	0.00
ATOM	53	O	LEU	A	528	33.997	-3.721	90.325	1.00	0.00
ATOM	54	N	THR	A	529	31.794	-3.278	90.447	1.00	0.00
ATOM	56	CA	THR	A	529	31.839	-2.254	89.408	1.00	0.00
ATOM	57	CB	THR	A	529	30.592	-2.393	88.540	1.00	0.00
ATOM	58	OG1	THR	A	529	30.607	-3.688	87.958	1.00	0.00

ATOM	59	CG2	THR	A	529	30.539	-1.366	87.417	1.00	0.00
ATOM	60	C	THR	A	529	31.883	-0.884	90.076	1.00	0.00
ATOM	61	O	THR	A	529	30.909	-0.470	90.718	1.00	0.00
ATOM	62	N	PRO	A	530	32.993	-0.185	89.887	1.00	0.00
ATOM	63	CA	PRO	A	530	33.234	1.104	90.544	1.00	0.00
ATOM	64	CB	PRO	A	530	34.571	1.567	90.055	1.00	0.00
ATOM	65	CG	PRO	A	530	35.165	0.505	89.148	1.00	0.00
ATOM	66	CD	PRO	A	530	34.140	-0.613	89.089	1.00	0.00
ATOM	67	C	PRO	A	530	32.150	2.125	90.236	1.00	0.00
ATOM	68	O	PRO	A	530	31.449	2.042	89.216	1.00	0.00
ATOM	69	N	THR	A	531	32.129	3.169	91.045	1.00	0.00
ATOM	71	CA	THR	A	531	31.052	4.162	90.968	1.00	0.00
ATOM	72	CB	THR	A	531	31.140	5.085	92.180	1.00	0.00
ATOM	73	OG1	THR	A	531	32.362	5.809	92.114	1.00	0.00
ATOM	74	CG2	THR	A	531	31.111	4.300	93.487	1.00	0.00
ATOM	75	C	THR	A	531	31.073	5.007	89.695	1.00	0.00
ATOM	76	O	THR	A	531	29.993	5.350	89.210	1.00	0.00
ATOM	77	N	LEU	A	532	32.208	5.125	89.025	1.00	0.00
ATOM	79	CA	LEU	A	532	32.214	5.894	87.780	1.00	0.00
ATOM	80	CB	LEU	A	532	33.573	6.565	87.618	1.00	0.00
ATOM	81	CG	LEU	A	532	33.609	7.529	86.435	1.00	0.00
ATOM	82	CD1	LEU	A	532	32.501	8.573	86.536	1.00	0.00
ATOM	83	CD2	LEU	A	532	34.970	8.206	86.334	1.00	0.00
ATOM	84	C	LEU	A	532	31.877	5.010	86.577	1.00	0.00
ATOM	85	O	LEU	A	532	31.237	5.497	85.639	1.00	0.00
ATOM	86	N	VAL	A	533	32.020	3.701	86.726	1.00	0.00
ATOM	88	CA	VAL	A	533	31.635	2.801	85.633	1.00	0.00
ATOM	89	CB	VAL	A	533	32.392	1.482	85.741	1.00	0.00
ATOM	90	CG1	VAL	A	533	31.996	0.549	84.604	1.00	0.00
ATOM	91	CG2	VAL	A	533	33.898	1.695	85.730	1.00	0.00
ATOM	92	C	VAL	A	533	30.137	2.530	85.710	1.00	0.00
ATOM	93	O	VAL	A	533	29.442	2.546	84.686	1.00	0.00
ATOM	94	N	SER	A	534	29.623	2.561	86.929	1.00	0.00
ATOM	96	CA	SER	A	534	28.178	2.440	87.121	1.00	0.00
ATOM	97	CB	SER	A	534	27.893	1.973	88.547	1.00	0.00
ATOM	98	OG	SER	A	534	28.439	2.917	89.458	1.00	0.00
ATOM	99	C	SER	A	534	27.479	3.769	86.836	1.00	0.00
ATOM	100	O	SER	A	534	26.379	3.756	86.274	1.00	0.00
ATOM	101	N	LEU	A	535	28.220	4.863	86.926	1.00	0.00
ATOM	103	CA	LEU	A	535	27.688	6.171	86.543	1.00	0.00
ATOM	104	CB	LEU	A	535	28.623	7.247	87.101	1.00	0.00
ATOM	105	CG	LEU	A	535	28.050	8.665	87.076	1.00	0.00
ATOM	106	CD1	LEU	A	535	28.691	9.518	88.164	1.00	0.00
ATOM	107	CD2	LEU	A	535	28.186	9.346	85.717	1.00	0.00

ATOM	108	C	LEU	A	535	27.595	6.254	85.025	1.00	0.00
ATOM	109	O	LEU	A	535	26.532	6.638	84.525	1.00	0.00
ATOM	110	N	LEU	A	536	28.530	5.617	84.333	1.00	0.00
ATOM	112	CA	LEU	A	536	28.472	5.531	82.867	1.00	0.00
ATOM	113	CB	LEU	A	536	29.718	4.810	82.361	1.00	0.00
ATOM	114	CG	LEU	A	536	30.987	5.631	82.524	1.00	0.00
ATOM	115	CD1	LEU	A	536	32.223	4.782	82.252	1.00	0.00
ATOM	116	CD2	LEU	A	536	30.958	6.847	81.611	1.00	0.00
ATOM	117	C	LEU	A	536	27.259	4.736	82.399	1.00	0.00
ATOM	118	O	LEU	A	536	26.520	5.207	81.527	1.00	0.00
ATOM	119	N	GLU	A	537	26.914	3.696	83.143	1.00	0.00
ATOM	121	CA	GLU	A	537	25.777	2.858	82.762	1.00	0.00
ATOM	122	CB	GLU	A	537	25.977	1.487	83.413	1.00	0.00
ATOM	123	CG	GLU	A	537	24.963	0.430	82.969	1.00	0.00
ATOM	124	CD	GLU	A	537	23.742	0.407	83.887	1.00	0.00
ATOM	125	OE1	GLU	A	537	23.842	1.014	84.946	1.00	0.00
ATOM	126	OE2	GLU	A	537	22.874	-0.419	83.642	1.00	0.00
ATOM	127	C	GLU	A	537	24.435	3.482	83.158	1.00	0.00
ATOM	128	O	GLU	A	537	23.419	3.143	82.541	1.00	0.00
ATOM	129	N	VAL	A	538	24.441	4.447	84.063	1.00	0.00
ATOM	131	CA	VAL	A	538	23.200	5.129	84.441	1.00	0.00
ATOM	132	CB	VAL	A	538	23.276	5.436	85.937	1.00	0.00
ATOM	133	CG1	VAL	A	538	22.137	6.333	86.412	1.00	0.00
ATOM	134	CG2	VAL	A	538	23.303	4.148	86.754	1.00	0.00
ATOM	135	C	VAL	A	538	22.971	6.409	83.627	1.00	0.00
ATOM	136	O	VAL	A	538	21.821	6.826	83.441	1.00	0.00
ATOM	137	N	ILE	A	539	24.032	6.969	83.066	1.00	0.00
ATOM	139	CA	ILE	A	539	23.872	8.155	82.212	1.00	0.00
ATOM	140	CB	ILE	A	539	24.957	9.187	82.534	1.00	0.00
ATOM	141	CG2	ILE	A	539	24.796	9.679	83.968	1.00	0.00
ATOM	142	CG1	ILE	A	539	26.386	8.700	82.303	1.00	0.00
ATOM	143	CD1	ILE	A	539	26.921	9.060	80.923	1.00	0.00
ATOM	144	C	ILE	A	539	23.823	7.782	80.730	1.00	0.00
ATOM	145	O	ILE	A	539	23.623	8.644	79.864	1.00	0.00
ATOM	146	N	GLU	A	540	24.011	6.501	80.459	1.00	0.00
ATOM	148	CA	GLU	A	540	23.833	5.941	79.118	1.00	0.00
ATOM	149	CB	GLU	A	540	24.149	4.449	79.241	1.00	0.00
ATOM	150	CG	GLU	A	540	24.286	3.751	77.894	1.00	0.00
ATOM	151	CD	GLU	A	540	25.492	4.312	77.147	1.00	0.00
ATOM	152	OE1	GLU	A	540	26.468	4.639	77.809	1.00	0.00
ATOM	153	OE2	GLU	A	540	25.402	4.442	75.935	1.00	0.00
ATOM	154	C	GLU	A	540	22.386	6.135	78.651	1.00	0.00
ATOM	155	O	GLU	A	540	21.446	5.834	79.392	1.00	0.00
ATOM	156	N	PRO	A	541	22.224	6.667	77.448	1.00	0.00

ATOM	157	CA	PRO A 541	20.897	6.933	76.878	1.00	0.00
ATOM	158	CB	PRO A 541	21.149	7.770	75.662	1.00	0.00
ATOM	159	CG	PRO A 541	22.646	7.839	75.408	1.00	0.00
ATOM	160	CD	PRO A 541	23.303	7.091	76.556	1.00	0.00
ATOM	161	C	PRO A 541	20.126	5.663	76.507	1.00	0.00
ATOM	162	O	PRO A 541	20.275	4.595	77.113	1.00	0.00
ATOM	163	N	GLU A 542	19.264	5.827	75.519	1.00	0.00
ATOM	165	CA	GLU A 542	18.347	4.761	75.107	1.00	0.00
ATOM	166	CB	GLU A 542	16.936	5.359	75.169	1.00	0.00
ATOM	167	CG	GLU A 542	15.810	4.352	74.940	1.00	0.00
ATOM	168	CD	GLU A 542	15.851	3.251	75.999	1.00	0.00
ATOM	169	OE1	GLU A 542	15.282	3.461	77.059	1.00	0.00
ATOM	170	OE2	GLU A 542	16.528	2.260	75.754	1.00	0.00
ATOM	171	C	GLU A 542	18.670	4.273	73.692	1.00	0.00
ATOM	172	O	GLU A 542	19.133	5.060	72.858	1.00	0.00
ATOM	173	N	VAL A 543	18.490	2.980	73.457	1.00	0.00
ATOM	175	CA	VAL A 543	18.560	2.443	72.092	1.00	0.00
ATOM	176	CB	VAL A 543	18.459	0.915	72.140	1.00	0.00
ATOM	177	CG1	VAL A 543	17.202	0.440	72.862	1.00	0.00
ATOM	178	CG2	VAL A 543	18.554	0.286	70.753	1.00	0.00
ATOM	179	C	VAL A 543	17.420	3.067	71.284	1.00	0.00
ATOM	180	O	VAL A 543	16.281	3.174	71.755	1.00	0.00
ATOM	181	N	LEU A 544	17.781	3.629	70.145	1.00	0.00
ATOM	183	CA	LEU A 544	16.825	4.430	69.382	1.00	0.00
ATOM	184	CB	LEU A 544	17.562	5.656	68.864	1.00	0.00
ATOM	185	CG	LEU A 544	18.042	6.512	70.029	1.00	0.00
ATOM	186	CD1	LEU A 544	19.047	7.556	69.573	1.00	0.00
ATOM	187	CD2	LEU A 544	16.872	7.155	70.766	1.00	0.00
ATOM	188	C	LEU A 544	16.180	3.683	68.227	1.00	0.00
ATOM	189	O	LEU A 544	16.693	2.676	67.728	1.00	0.00
ATOM	190	N	TYR A 545	14.965	4.108	67.936	1.00	0.00
ATOM	192	CA	TYR A 545	14.260	3.652	66.740	1.00	0.00
ATOM	193	CB	TYR A 545	12.757	3.789	66.965	1.00	0.00
ATOM	194	CG	TYR A 545	12.247	3.056	68.206	1.00	0.00
ATOM	195	CD1	TYR A 545	11.731	3.778	69.276	1.00	0.00
ATOM	196	CE1	TYR A 545	11.275	3.116	70.408	1.00	0.00
ATOM	197	CZ	TYR A 545	11.333	1.730	70.467	1.00	0.00
ATOM	198	OH	TYR A 545	10.913	1.073	71.603	1.00	0.00
ATOM	199	CE2	TYR A 545	11.838	1.004	69.396	1.00	0.00
ATOM	200	CD2	TYR A 545	12.294	1.668	68.264	1.00	0.00
ATOM	201	C	TYR A 545	14.710	4.509	65.561	1.00	0.00
ATOM	202	O	TYR A 545	14.930	5.715	65.709	1.00	0.00
ATOM	203	N	ALA A 546	14.804	3.894	64.394	1.00	0.00
ATOM	205	CA	ALA A 546	15.305	4.594	63.202	1.00	0.00

ATOM	206	CB	ALA A 546	15.917	3.562	62.265	1.00	0.00
ATOM	207	C	ALA A 546	14.225	5.362	62.447	1.00	0.00
ATOM	208	O	ALA A 546	14.527	6.166	61.557	1.00	0.00
ATOM	209	N	GLY A 547	12.977	5.107	62.802	1.00	0.00
ATOM	211	CA	GLY A 547	11.850	5.753	62.127	1.00	0.00
ATOM	212	C	GLY A 547	11.509	4.995	60.851	1.00	0.00
ATOM	213	O	GLY A 547	11.063	5.577	59.856	1.00	0.00
ATOM	214	N	TYR A 548	11.748	3.695	60.882	1.00	0.00
ATOM	216	CA	TYR A 548	11.488	2.869	59.708	1.00	0.00
ATOM	217	CB	TYR A 548	12.402	1.648	59.769	1.00	0.00
ATOM	218	CG	TYR A 548	12.421	0.853	58.473	1.00	0.00
ATOM	219	CD1	TYR A 548	12.358	1.532	57.263	1.00	0.00
ATOM	220	CE1	TYR A 548	12.351	0.827	56.071	1.00	0.00
ATOM	221	CZ	TYR A 548	12.421	-0.558	56.092	1.00	0.00
ATOM	222	OH	TYR A 548	12.386	-1.249	54.905	1.00	0.00
ATOM	223	CE2	TYR A 548	12.507	-1.242	57.298	1.00	0.00
ATOM	224	CD2	TYR A 548	12.509	-0.533	58.493	1.00	0.00
ATOM	225	C	TYR A 548	10.018	2.457	59.680	1.00	0.00
ATOM	226	O	TYR A 548	9.464	2.010	60.690	1.00	0.00
ATOM	227	N	ASP A 549	9.403	2.586	58.512	1.00	0.00
ATOM	229	CA	ASP A 549	7.982	2.238	58.349	1.00	0.00
ATOM	230	CB	ASP A 549	7.420	2.999	57.152	1.00	0.00
ATOM	231	CG	ASP A 549	7.556	4.508	57.353	1.00	0.00
ATOM	232	OD1	ASP A 549	6.803	5.048	58.149	1.00	0.00
ATOM	233	OD2	ASP A 549	8.414	5.085	56.700	1.00	0.00
ATOM	234	C	ASP A 549	7.753	0.735	58.152	1.00	0.00
ATOM	235	O	ASP A 549	6.596	0.294	58.159	1.00	0.00
ATOM	236	N	SER A 550	8.824	0.003	57.862	1.00	0.00
ATOM	238	CA	SER A 550	8.898	-1.480	57.888	1.00	0.00
ATOM	239	CB	SER A 550	8.434	-1.940	59.266	1.00	0.00
ATOM	240	OG	SER A 550	8.472	-3.360	59.288	1.00	0.00
ATOM	241	C	SER A 550	8.143	-2.292	56.818	1.00	0.00
ATOM	242	O	SER A 550	8.621	-3.367	56.439	1.00	0.00
ATOM	243	N	SER A 551	7.012	-1.814	56.330	1.00	0.00
ATOM	245	CA	SER A 551	6.255	-2.568	55.326	1.00	0.00
ATOM	246	CB	SER A 551	4.779	-2.238	55.500	1.00	0.00
ATOM	247	OG	SER A 551	4.424	-2.568	56.836	1.00	0.00
ATOM	248	C	SER A 551	6.695	-2.216	53.912	1.00	0.00
ATOM	249	O	SER A 551	6.514	-3.002	52.976	1.00	0.00
ATOM	250	N	VAL A 552	7.313	-1.057	53.778	1.00	0.00
ATOM	252	CA	VAL A 552	7.876	-0.656	52.491	1.00	0.00
ATOM	253	CB	VAL A 552	7.800	0.869	52.387	1.00	0.00
ATOM	254	CG1	VAL A 552	8.416	1.566	53.596	1.00	0.00
ATOM	255	CG2	VAL A 552	8.402	1.388	51.086	1.00	0.00

ATOM	256	C	VAL	A	552	9.313	-1.167	52.375	1.00	0.00
ATOM	257	O	VAL	A	552	10.136	-0.946	53.272	1.00	0.00
ATOM	258	N	PRO	A	553	9.580	-1.907	51.310	1.00	0.00
ATOM	259	CA	PRO	A	553	10.933	-2.405	51.049	1.00	0.00
ATOM	260	CB	PRO	A	553	10.815	-3.246	49.816	1.00	0.00
ATOM	261	CG	PRO	A	553	9.387	-3.180	49.297	1.00	0.00
ATOM	262	CD	PRO	A	553	8.625	-2.294	50.269	1.00	0.00
ATOM	263	C	PRO	A	553	11.909	-1.251	50.850	1.00	0.00
ATOM	264	O	PRO	A	553	11.602	-0.258	50.179	1.00	0.00
ATOM	265	N	ASP	A	554	13.067	-1.376	51.474	1.00	0.00
ATOM	267	CA	ASP	A	554	14.087	-0.329	51.374	1.00	0.00
ATOM	268	CB	ASP	A	554	15.171	-0.550	52.421	1.00	0.00
ATOM	269	CG	ASP	A	554	14.847	0.260	53.667	1.00	0.00
ATOM	270	OD1	ASP	A	554	14.195	1.281	53.512	1.00	0.00
ATOM	271	OD2	ASP	A	554	15.249	-0.162	54.740	1.00	0.00
ATOM	272	C	ASP	A	554	14.761	-0.252	50.016	1.00	0.00
ATOM	273	O	ASP	A	554	15.494	-1.154	49.596	1.00	0.00
ATOM	274	N	SER	A	555	14.485	0.844	49.334	1.00	0.00
ATOM	276	CA	SER	A	555	15.327	1.251	48.211	1.00	0.00
ATOM	277	CB	SER	A	555	14.626	2.330	47.398	1.00	0.00
ATOM	278	OG	SER	A	555	14.660	3.522	48.172	1.00	0.00
ATOM	279	C	SER	A	555	16.577	1.853	48.831	1.00	0.00
ATOM	280	O	SER	A	555	16.568	2.154	50.032	1.00	0.00
ATOM	281	N	THR	A	556	17.572	2.174	48.023	1.00	0.00
ATOM	283	CA	THR	A	556	18.768	2.801	48.593	1.00	0.00
ATOM	284	CB	THR	A	556	19.911	2.769	47.583	1.00	0.00
ATOM	285	OG1	THR	A	556	20.919	3.637	48.084	1.00	0.00
ATOM	286	CG2	THR	A	556	19.499	3.272	46.202	1.00	0.00
ATOM	287	C	THR	A	556	18.499	4.234	49.061	1.00	0.00
ATOM	288	O	THR	A	556	18.986	4.614	50.132	1.00	0.00
ATOM	289	N	TRP	A	557	17.501	4.873	48.472	1.00	0.00
ATOM	291	CA	TRP	A	557	17.101	6.209	48.911	1.00	0.00
ATOM	292	CB	TRP	A	557	16.147	6.804	47.878	1.00	0.00
ATOM	293	CG	TRP	A	557	16.685	6.926	46.461	1.00	0.00
ATOM	294	CD1	TRP	A	557	18.000	6.960	46.052	1.00	0.00
ATOM	295	NE1	TRP	A	557	18.034	7.100	44.704	1.00	0.00
ATOM	297	CE2	TRP	A	557	16.792	7.152	44.193	1.00	0.00
ATOM	298	CZ2	TRP	A	557	16.313	7.298	42.899	1.00	0.00
ATOM	299	CH2	TRP	A	557	14.940	7.321	42.671	1.00	0.00
ATOM	300	CZ3	TRP	A	557	14.050	7.198	43.732	1.00	0.00
ATOM	301	CE3	TRP	A	557	14.521	7.054	45.031	1.00	0.00
ATOM	302	CD2	TRP	A	557	15.887	7.032	45.261	1.00	0.00
ATOM	303	C	TRP	A	557	16.387	6.134	50.259	1.00	0.00
ATOM	304	O	TRP	A	557	16.803	6.803	51.212	1.00	0.00

ATOM	305	N	ARG A 558	15.517	5.145	50.411	1.00	0.00
ATOM	307	CA	ARG A 558	14.791	4.994	51.677	1.00	0.00
ATOM	308	CB	ARG A 558	13.663	3.993	51.479	1.00	0.00
ATOM	309	CG	ARG A 558	12.693	4.469	50.410	1.00	0.00
ATOM	310	CD	ARG A 558	11.557	3.471	50.217	1.00	0.00
ATOM	311	NE	ARG A 558	10.668	3.894	49.123	1.00	0.00
ATOM	312	CZ	ARG A 558	9.544	4.594	49.306	1.00	0.00
ATOM	313	NH1	ARG A 558	9.164	4.950	50.538	1.00	0.00
ATOM	314	NH2	ARG A 558	8.795	4.935	48.255	1.00	0.00
ATOM	315	C	ARG A 558	15.668	4.520	52.832	1.00	0.00
ATOM	316	O	ARG A 558	15.528	5.062	53.936	1.00	0.00
ATOM	317	N	ILE A 559	16.703	3.742	52.556	1.00	0.00
ATOM	319	CA	ILE A 559	17.563	3.325	53.663	1.00	0.00
ATOM	320	CB	ILE A 559	18.271	2.004	53.340	1.00	0.00
ATOM	321	CG2	ILE A 559	19.157	2.093	52.105	1.00	0.00
ATOM	322	CG1	ILE A 559	19.092	1.516	54.529	1.00	0.00
ATOM	323	CD1	ILE A 559	18.210	1.234	55.740	1.00	0.00
ATOM	324	C	ILE A 559	18.542	4.439	54.047	1.00	0.00
ATOM	325	O	ILE A 559	18.731	4.655	55.250	1.00	0.00
ATOM	326	N	MET A 560	18.863	5.331	53.121	1.00	0.00
ATOM	328	CA	MET A 560	19.720	6.457	53.488	1.00	0.00
ATOM	329	CB	MET A 560	20.376	7.042	52.243	1.00	0.00
ATOM	330	CG	MET A 560	21.336	6.047	51.603	1.00	0.00
ATOM	331	SD	MET A 560	22.247	6.663	50.168	1.00	0.00
ATOM	332	CE	MET A 560	20.856	7.241	49.168	1.00	0.00
ATOM	333	C	MET A 560	18.926	7.539	54.207	1.00	0.00
ATOM	334	O	MET A 560	19.406	8.049	55.224	1.00	0.00
ATOM	335	N	THR A 561	17.649	7.665	53.885	1.00	0.00
ATOM	337	CA	THR A 561	16.813	8.653	54.580	1.00	0.00
ATOM	338	CB	THR A 561	15.599	9.005	53.725	1.00	0.00
ATOM	339	OG1	THR A 561	14.891	7.812	53.416	1.00	0.00
ATOM	340	CG2	THR A 561	16.008	9.669	52.418	1.00	0.00
ATOM	341	C	THR A 561	16.358	8.187	55.966	1.00	0.00
ATOM	342	O	THR A 561	16.308	9.019	56.881	1.00	0.00
ATOM	343	N	THR A 562	16.273	6.886	56.203	1.00	0.00
ATOM	345	CA	THR A 562	15.961	6.459	57.573	1.00	0.00
ATOM	346	CB	THR A 562	15.204	5.130	57.599	1.00	0.00
ATOM	347	OG1	THR A 562	14.894	4.838	58.957	1.00	0.00
ATOM	348	CG2	THR A 562	16.002	3.962	57.033	1.00	0.00
ATOM	349	C	THR A 562	17.230	6.403	58.422	1.00	0.00
ATOM	350	O	THR A 562	17.162	6.627	59.636	1.00	0.00
ATOM	351	N	LEU A 563	18.384	6.388	57.770	1.00	0.00
ATOM	353	CA	LEU A 563	19.644	6.547	58.498	1.00	0.00
ATOM	354	CB	LEU A 563	20.762	5.840	57.741	1.00	0.00

ATOM	355	CG	LEU A 563	20.561	4.329	57.757	1.00	0.00
ATOM	356	CD1	LEU A 563	21.617	3.623	56.914	1.00	0.00
ATOM	357	CD2	LEU A 563	20.559	3.794	59.184	1.00	0.00
ATOM	358	C	LEU A 563	19.986	8.023	58.694	1.00	0.00
ATOM	359	O	LEU A 563	20.776	8.359	59.581	1.00	0.00
ATOM	360	N	ASN A 564	19.291	8.899	57.987	1.00	0.00
ATOM	362	CA	ASN A 564	19.408	10.340	58.231	1.00	0.00
ATOM	363	CB	ASN A 564	18.891	11.101	57.012	1.00	0.00
ATOM	364	CG	ASN A 564	19.845	11.032	55.820	1.00	0.00
ATOM	365	OD1	ASN A 564	19.410	11.086	54.658	1.00	0.00
ATOM	366	ND2	ASN A 564	21.132	11.072	56.120	1.00	0.00
ATOM	369	C	ASN A 564	18.562	10.738	59.432	1.00	0.00
ATOM	370	O	ASN A 564	19.003	11.535	60.274	1.00	0.00
ATOM	371	N	MET A 565	17.446	10.045	59.595	1.00	0.00
ATOM	373	CA	MET A 565	16.570	10.286	60.742	1.00	0.00
ATOM	374	CB	MET A 565	15.213	9.662	60.441	1.00	0.00
ATOM	375	CG	MET A 565	14.193	10.003	61.520	1.00	0.00
ATOM	376	SD	MET A 565	13.873	11.769	61.731	1.00	0.00
ATOM	377	CE	MET A 565	13.319	12.168	60.056	1.00	0.00
ATOM	378	C	MET A 565	17.158	9.662	62.003	1.00	0.00
ATOM	379	O	MET A 565	17.307	10.352	63.021	1.00	0.00
ATOM	380	N	LEU A 566	17.734	8.481	61.847	1.00	0.00
ATOM	382	CA	LEU A 566	18.408	7.825	62.971	1.00	0.00
ATOM	383	CB	LEU A 566	18.670	6.378	62.581	1.00	0.00
ATOM	384	CG	LEU A 566	19.330	5.598	63.709	1.00	0.00
ATOM	385	CD1	LEU A 566	18.467	5.589	64.967	1.00	0.00
ATOM	386	CD2	LEU A 566	19.635	4.179	63.257	1.00	0.00
ATOM	387	C	LEU A 566	19.727	8.514	63.320	1.00	0.00
ATOM	388	O	LEU A 566	20.020	8.674	64.510	1.00	0.00
ATOM	389	N	GLY A 567	20.361	9.125	62.332	1.00	0.00
ATOM	391	CA	GLY A 567	21.553	9.948	62.554	1.00	0.00
ATOM	392	C	GLY A 567	21.234	11.124	63.467	1.00	0.00
ATOM	393	O	GLY A 567	21.854	11.263	64.527	1.00	0.00
ATOM	394	N	GLY A 568	20.165	11.840	63.150	1.00	0.00
ATOM	396	CA	GLY A 568	19.707	12.956	63.986	1.00	0.00
ATOM	397	C	GLY A 568	19.314	12.517	65.396	1.00	0.00
ATOM	398	O	GLY A 568	19.749	13.140	66.375	1.00	0.00
ATOM	399	N	ARG A 569	18.646	11.378	65.501	1.00	0.00
ATOM	401	CA	ARG A 569	18.287	10.823	66.814	1.00	0.00
ATOM	402	CB	ARG A 569	17.431	9.576	66.607	1.00	0.00
ATOM	403	CG	ARG A 569	16.096	9.914	65.955	1.00	0.00
ATOM	404	CD	ARG A 569	15.301	10.883	66.824	1.00	0.00
ATOM	405	NE	ARG A 569	14.045	11.279	66.170	1.00	0.00
ATOM	406	CZ	ARG A 569	13.861	12.476	65.610	1.00	0.00

ATOM	407	NH1	ARG	A	569	14.862	13.359	65.576	1.00	0.00
ATOM	408	NH2	ARG	A	569	12.686	12.778	65.055	1.00	0.00
ATOM	409	C	ARG	A	569	19.514	10.442	67.645	1.00	0.00
ATOM	410	O	ARG	A	569	19.581	10.806	68.826	1.00	0.00
ATOM	411	N	GLN	A	570	20.552	9.933	67.003	1.00	0.00
ATOM	413	CA	GLN	A	570	21.776	9.590	67.729	1.00	0.00
ATOM	414	CB	GLN	A	570	22.581	8.600	66.900	1.00	0.00
ATOM	415	CG	GLN	A	570	21.822	7.289	66.733	1.00	0.00
ATOM	416	CD	GLN	A	570	22.624	6.329	65.864	1.00	0.00
ATOM	417	OE1	GLN	A	570	22.360	6.182	64.665	1.00	0.00
ATOM	418	NE2	GLN	A	570	23.624	5.716	66.473	1.00	0.00
ATOM	421	C	GLN	A	570	22.630	10.813	68.041	1.00	0.00
ATOM	422	O	GLN	A	570	23.319	10.806	69.065	1.00	0.00
ATOM	423	N	VAL	A	571	22.418	11.909	67.331	1.00	0.00
ATOM	425	CA	VAL	A	571	23.112	13.154	67.664	1.00	0.00
ATOM	426	CB	VAL	A	571	23.083	14.085	66.455	1.00	0.00
ATOM	427	CG1	VAL	A	571	23.572	15.482	66.818	1.00	0.00
ATOM	428	CG2	VAL	A	571	23.896	13.518	65.298	1.00	0.00
ATOM	429	C	VAL	A	571	22.462	13.844	68.858	1.00	0.00
ATOM	430	O	VAL	A	571	23.181	14.252	69.780	1.00	0.00
ATOM	431	N	ILE	A	572	21.149	13.728	68.986	1.00	0.00
ATOM	433	CA	ILE	A	572	20.496	14.356	70.137	1.00	0.00
ATOM	434	CB	ILE	A	572	19.057	14.749	69.756	1.00	0.00
ATOM	435	CG2	ILE	A	572	18.171	13.538	69.493	1.00	0.00
ATOM	436	CG1	ILE	A	572	18.387	15.664	70.784	1.00	0.00
ATOM	437	CD1	ILE	A	572	17.740	14.905	71.940	1.00	0.00
ATOM	438	C	ILE	A	572	20.613	13.460	71.378	1.00	0.00
ATOM	439	O	ILE	A	572	20.808	13.986	72.481	1.00	0.00
ATOM	440	N	ALA	A	573	20.826	12.169	71.170	1.00	0.00
ATOM	442	CA	ALA	A	573	21.104	11.288	72.304	1.00	0.00
ATOM	443	CB	ALA	A	573	20.788	9.851	71.907	1.00	0.00
ATOM	444	C	ALA	A	573	22.564	11.389	72.735	1.00	0.00
ATOM	445	O	ALA	A	573	22.844	11.360	73.939	1.00	0.00
ATOM	446	N	ALA	A	574	23.431	11.768	71.809	1.00	0.00
ATOM	448	CA	ALA	A	574	24.844	11.946	72.137	1.00	0.00
ATOM	449	CB	ALA	A	574	25.679	11.832	70.868	1.00	0.00
ATOM	450	C	ALA	A	574	25.115	13.288	72.800	1.00	0.00
ATOM	451	O	ALA	A	574	25.967	13.344	73.691	1.00	0.00
ATOM	452	N	VAL	A	575	24.280	14.287	72.556	1.00	0.00
ATOM	454	CA	VAL	A	575	24.466	15.544	73.284	1.00	0.00
ATOM	455	CB	VAL	A	575	23.973	16.736	72.457	1.00	0.00
ATOM	456	CG1	VAL	A	575	22.492	16.662	72.109	1.00	0.00
ATOM	457	CG2	VAL	A	575	24.283	18.056	73.154	1.00	0.00
ATOM	458	C	VAL	A	575	23.794	15.479	74.657	1.00	0.00

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ATOM    459  O   VAL A 575      24.335  16.042  75.617  1.00  0.00
ATOM    460  N   LYS A 576      22.851  14.561  74.817  1.00  0.00
ATOM    462  CA  LYS A 576      22.260  14.340  76.136  1.00  0.00
ATOM    463  CB  LYS A 576      20.923  13.631  75.954  1.00  0.00
ATOM    464  CG  LYS A 576      20.179  13.495  77.277  1.00  0.00
ATOM    465  CD  LYS A 576      19.845  14.863  77.866  1.00  0.00
ATOM    466  CE  LYS A 576      18.933  15.661  76.940  1.00  0.00
ATOM    467  NZ  LYS A 576      18.649  16.992  77.502  1.00  0.00
ATOM    468  C   LYS A 576      23.192  13.489  76.996  1.00  0.00
ATOM    469  O   LYS A 576      23.433  13.827  78.161  1.00  0.00
ATOM    470  N   TRP A 577      23.921  12.600  76.341  1.00  0.00
ATOM    472  CA  TRP A 577      24.933  11.783  77.016  1.00  0.00
ATOM    473  CB  TRP A 577      25.275  10.636  76.070  1.00  0.00
ATOM    474  CG  TRP A 577      26.408   9.734  76.514  1.00  0.00
ATOM    475  CD1 TRP A 577      26.335   8.699  77.416  1.00  0.00
ATOM    476  NE1 TRP A 577      27.566   8.143  77.534  1.00  0.00
ATOM    478  CE2 TRP A 577      28.459   8.765  76.744  1.00  0.00
ATOM    479  CZ2 TRP A 577      29.818   8.580  76.527  1.00  0.00
ATOM    480  CH2 TRP A 577      30.489   9.395  75.623  1.00  0.00
ATOM    481  CZ3 TRP A 577      29.809  10.396  74.939  1.00  0.00
ATOM    482  CE3 TRP A 577      28.451  10.596  75.156  1.00  0.00
ATOM    483  CD2 TRP A 577      27.778   9.786  76.059  1.00  0.00
ATOM    484  C   TRP A 577      26.189  12.595  77.335  1.00  0.00
ATOM    485  O   TRP A 577      26.751  12.448  78.427  1.00  0.00
ATOM    486  N   ALA A 578      26.443  13.617  76.534  1.00  0.00
ATOM    488  CA  ALA A 578      27.569  14.521  76.777  1.00  0.00
ATOM    489  CB  ALA A 578      27.869  15.253  75.477  1.00  0.00
ATOM    490  C   ALA A 578      27.265  15.526  77.887  1.00  0.00
ATOM    491  O   ALA A 578      28.163  15.909  78.642  1.00  0.00
ATOM    492  N   LYS A 579      25.986  15.774  78.112  1.00  0.00
ATOM    494  CA  LYS A 579      25.557  16.603  79.243  1.00  0.00
ATOM    495  CB  LYS A 579      24.318  17.406  78.849  1.00  0.00
ATOM    496  CG  LYS A 579      24.591  18.882  78.523  1.00  0.00
ATOM    497  CD  LYS A 579      25.272  19.154  77.177  1.00  0.00
ATOM    498  CE  LYS A 579      26.797  19.067  77.221  1.00  0.00
ATOM    499  NZ  LYS A 579      27.364  20.023  78.184  1.00  0.00
ATOM    500  C   LYS A 579      25.264  15.765  80.489  1.00  0.00
ATOM    501  O   LYS A 579      24.777  16.293  81.496  1.00  0.00
ATOM    502  N   ALA A 580      25.488  14.466  80.394  1.00  0.00
ATOM    504  CA  ALA A 580      25.344  13.584  81.548  1.00  0.00
ATOM    505  CB  ALA A 580      24.418  12.440  81.155  1.00  0.00
ATOM    506  C   ALA A 580      26.699  13.040  81.996  1.00  0.00
ATOM    507  O   ALA A 580      26.812  12.466  83.087  1.00  0.00
ATOM    508  N   ILE A 581      27.712  13.222  81.164  1.00  0.00
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ATOM	510	CA	ILE	A	581	29.057	12.754	81.513	1.00	0.00
ATOM	511	CB	ILE	A	581	29.733	12.233	80.235	1.00	0.00
ATOM	512	CG2	ILE	A	581	29.876	13.305	79.168	1.00	0.00
ATOM	513	CG1	ILE	A	581	31.085	11.594	80.507	1.00	0.00
ATOM	514	CD1	ILE	A	581	30.914	10.291	81.274	1.00	0.00
ATOM	515	C	ILE	A	581	29.872	13.854	82.211	1.00	0.00
ATOM	516	O	ILE	A	581	30.131	14.936	81.664	1.00	0.00
ATOM	517	N	PRO	A	582	30.282	13.547	83.432	1.00	0.00
ATOM	518	CA	PRO	A	582	31.176	14.428	84.187	1.00	0.00
ATOM	519	CB	PRO	A	582	31.409	13.739	85.496	1.00	0.00
ATOM	520	CG	PRO	A	582	30.686	12.401	85.493	1.00	0.00
ATOM	521	CD	PRO	A	582	29.980	12.307	84.151	1.00	0.00
ATOM	522	C	PRO	A	582	32.481	14.642	83.430	1.00	0.00
ATOM	523	O	PRO	A	582	32.879	13.809	82.607	1.00	0.00
ATOM	524	N	GLY	A	583	33.036	15.832	83.566	1.00	0.00
ATOM	526	CA	GLY	A	583	34.260	16.168	82.837	1.00	0.00
ATOM	527	C	GLY	A	583	33.958	16.979	81.579	1.00	0.00
ATOM	528	O	GLY	A	583	34.499	18.078	81.396	1.00	0.00
ATOM	529	N	PHE	A	584	33.011	16.502	80.783	1.00	0.00
ATOM	531	CA	PHE	A	584	32.704	17.165	79.513	1.00	0.00
ATOM	532	CB	PHE	A	584	31.836	16.235	78.682	1.00	0.00
ATOM	533	CG	PHE	A	584	31.544	16.728	77.270	1.00	0.00
ATOM	534	CD1	PHE	A	584	32.456	16.481	76.254	1.00	0.00
ATOM	535	CE1	PHE	A	584	32.187	16.910	74.962	1.00	0.00
ATOM	536	CZ	PHE	A	584	31.011	17.593	74.688	1.00	0.00
ATOM	537	CE2	PHE	A	584	30.109	17.860	75.708	1.00	0.00
ATOM	538	CD2	PHE	A	584	30.377	17.430	77.001	1.00	0.00
ATOM	539	C	PHE	A	584	31.976	18.478	79.752	1.00	0.00
ATOM	540	O	PHE	A	584	32.399	19.506	79.207	1.00	0.00
ATOM	541	N	ARG	A	585	31.186	18.502	80.814	1.00	0.00
ATOM	543	CA	ARG	A	585	30.507	19.733	81.240	1.00	0.00
ATOM	544	CB	ARG	A	585	29.345	19.333	82.131	1.00	0.00
ATOM	545	CG	ARG	A	585	28.432	18.343	81.426	1.00	0.00
ATOM	546	CD	ARG	A	585	27.286	17.947	82.343	1.00	0.00
ATOM	547	NE	ARG	A	585	27.795	17.323	83.574	1.00	0.00
ATOM	548	CZ	ARG	A	585	27.390	17.697	84.789	1.00	0.00
ATOM	549	NH1	ARG	A	585	26.498	18.681	84.920	1.00	0.00
ATOM	550	NH2	ARG	A	585	27.886	17.096	85.873	1.00	0.00
ATOM	551	C	ARG	A	585	31.414	20.686	82.026	1.00	0.00
ATOM	552	O	ARG	A	585	30.976	21.769	82.426	1.00	0.00
ATOM	553	N	ASN	A	586	32.657	20.285	82.241	1.00	0.00
ATOM	555	CA	ASN	A	586	33.616	21.107	82.973	1.00	0.00
ATOM	556	CB	ASN	A	586	34.311	20.210	83.992	1.00	0.00
ATOM	557	CG	ASN	A	586	33.266	19.620	84.938	1.00	0.00

ATOM	558	OD1	ASN	A	586	32.806	18.480	84.772	1.00	0.00
ATOM	559	ND2	ASN	A	586	32.846	20.442	85.882	1.00	0.00
ATOM	562	C	ASN	A	586	34.619	21.717	81.997	1.00	0.00
ATOM	563	O	ASN	A	586	35.348	22.658	82.337	1.00	0.00
ATOM	564	N	LEU	A	587	34.618	21.187	80.783	1.00	0.00
ATOM	566	CA	LEU	A	587	35.398	21.759	79.679	1.00	0.00
ATOM	567	CB	LEU	A	587	35.372	20.789	78.503	1.00	0.00
ATOM	568	CG	LEU	A	587	36.045	19.467	78.838	1.00	0.00
ATOM	569	CD1	LEU	A	587	35.842	18.453	77.720	1.00	0.00
ATOM	570	CD2	LEU	A	587	37.526	19.678	79.110	1.00	0.00
ATOM	571	C	LEU	A	587	34.792	23.075	79.216	1.00	0.00
ATOM	572	O	LEU	A	587	33.635	23.381	79.521	1.00	0.00
ATOM	573	N	HIS	A	588	35.584	23.846	78.490	1.00	0.00
ATOM	575	CA	HIS	A	588	35.078	25.082	77.877	1.00	0.00
ATOM	576	CB	HIS	A	588	36.258	25.795	77.222	1.00	0.00
ATOM	577	CG	HIS	A	588	35.913	27.059	76.463	1.00	0.00
ATOM	578	ND1	HIS	A	588	36.161	27.298	75.163	1.00	0.00
ATOM	580	CE1	HIS	A	588	35.694	28.526	74.849	1.00	0.00
ATOM	581	NE2	HIS	A	588	35.158	29.064	75.965	1.00	0.00
ATOM	582	CD2	HIS	A	588	35.292	28.175	76.973	1.00	0.00
ATOM	583	C	HIS	A	588	33.995	24.730	76.853	1.00	0.00
ATOM	584	O	HIS	A	588	34.136	23.734	76.133	1.00	0.00
ATOM	585	N	LEU	A	589	32.998	25.592	76.706	1.00	0.00
ATOM	587	CA	LEU	A	589	31.819	25.293	75.877	1.00	0.00
ATOM	588	CB	LEU	A	589	30.798	26.405	76.119	1.00	0.00
ATOM	589	CG	LEU	A	589	29.468	26.173	75.404	1.00	0.00
ATOM	590	CD1	LEU	A	589	28.292	26.500	76.318	1.00	0.00
ATOM	591	CD2	LEU	A	589	29.373	26.957	74.097	1.00	0.00
ATOM	592	C	LEU	A	589	32.119	25.144	74.382	1.00	0.00
ATOM	593	O	LEU	A	589	31.635	24.185	73.770	1.00	0.00
ATOM	594	N	ASP	A	590	33.128	25.841	73.881	1.00	0.00
ATOM	596	CA	ASP	A	590	33.489	25.662	72.466	1.00	0.00
ATOM	597	CB	ASP	A	590	34.272	26.871	71.966	1.00	0.00
ATOM	598	CG	ASP	A	590	33.418	28.137	72.020	1.00	0.00
ATOM	599	OD1	ASP	A	590	32.206	28.017	71.906	1.00	0.00
ATOM	600	OD2	ASP	A	590	33.989	29.191	72.256	1.00	0.00
ATOM	601	C	ASP	A	590	34.313	24.390	72.254	1.00	0.00
ATOM	602	O	ASP	A	590	34.208	23.760	71.194	1.00	0.00
ATOM	603	N	ASP	A	591	34.855	23.863	73.341	1.00	0.00
ATOM	605	CA	ASP	A	591	35.599	22.607	73.273	1.00	0.00
ATOM	606	CB	ASP	A	591	36.581	22.508	74.432	1.00	0.00
ATOM	607	CG	ASP	A	591	37.570	23.665	74.440	1.00	0.00
ATOM	608	OD1	ASP	A	591	37.852	24.229	73.392	1.00	0.00
ATOM	609	OD2	ASP	A	591	38.072	23.970	75.512	1.00	0.00

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ATOM    610  C   ASP A 591      34.624  21.448  73.385  1.00  0.00
ATOM    611  O   ASP A 591      34.844  20.408  72.759  1.00  0.00
ATOM    612  N   GLN A 592      33.473  21.710  73.984  1.00  0.00
ATOM    614  CA  GLN A 592      32.406  20.714  74.060  1.00  0.00
ATOM    615  CB  GLN A 592      31.336  21.222  75.015  1.00  0.00
ATOM    616  CG  GLN A 592      31.875  21.427  76.421  1.00  0.00
ATOM    617  CD  GLN A 592      30.825  22.143  77.264  1.00  0.00
ATOM    618  OE1 GLN A 592      29.914  22.790  76.735  1.00  0.00
ATOM    619  NE2 GLN A 592      30.989  22.043  78.568  1.00  0.00
ATOM    622  C   GLN A 592      31.776  20.539  72.690  1.00  0.00
ATOM    623  O   GLN A 592      31.686  19.408  72.189  1.00  0.00
ATOM    624  N   MET A 593      31.592  21.662  72.013  1.00  0.00
ATOM    626  CA  MET A 593      31.067  21.654  70.647  1.00  0.00
ATOM    627  CB  MET A 593      30.972  23.090  70.151  1.00  0.00
ATOM    628  CG  MET A 593      29.986  23.908  70.975  1.00  0.00
ATOM    629  SD  MET A 593      29.862  25.647  70.499  1.00  0.00
ATOM    630  CE  MET A 593      29.469  25.427  68.748  1.00  0.00
ATOM    631  C   MET A 593      31.986  20.873  69.722  1.00  0.00
ATOM    632  O   MET A 593      31.611  19.767  69.308  1.00  0.00
ATOM    633  N   THR A 594      33.252  21.260  69.701  1.00  0.00
ATOM    635  CA  THR A 594      34.221  20.615  68.803  1.00  0.00
ATOM    636  CB  THR A 594      35.519  21.417  68.818  1.00  0.00
ATOM    637  OG1 THR A 594      35.986  21.505  70.160  1.00  0.00
ATOM    638  CG2 THR A 594      35.308  22.832  68.291  1.00  0.00
ATOM    639  C   THR A 594      34.532  19.161  69.161  1.00  0.00
ATOM    640  O   THR A 594      34.664  18.345  68.243  1.00  0.00
ATOM    641  N   LEU A 595      34.388  18.783  70.419  1.00  0.00
ATOM    643  CA  LEU A 595      34.655  17.401  70.820  1.00  0.00
ATOM    644  CB  LEU A 595      34.707  17.349  72.337  1.00  0.00
ATOM    645  CG  LEU A 595      36.035  16.810  72.841  1.00  0.00
ATOM    646  CD1 LEU A 595      37.207  17.620  72.297  1.00  0.00
ATOM    647  CD2 LEU A 595      36.047  16.782  74.363  1.00  0.00
ATOM    648  C   LEU A 595      33.548  16.476  70.345  1.00  0.00
ATOM    649  O   LEU A 595      33.821  15.528  69.594  1.00  0.00
ATOM    650  N   LEU A 596      32.317  16.934  70.504  1.00  0.00
ATOM    652  CA  LEU A 596      31.168  16.125  70.099  1.00  0.00
ATOM    653  CB  LEU A 596      29.917  16.724  70.731  1.00  0.00
ATOM    654  CG  LEU A 596      28.678  15.888  70.432  1.00  0.00
ATOM    655  CD1 LEU A 596      28.811  14.485  71.015  1.00  0.00
ATOM    656  CD2 LEU A 596      27.427  16.570  70.970  1.00  0.00
ATOM    657  C   LEU A 596      31.020  16.111  68.582  1.00  0.00
ATOM    658  O   LEU A 596      30.764  15.046  68.007  1.00  0.00
ATOM    659  N   GLN A 597      31.458  17.181  67.940  1.00  0.00
ATOM    661  CA  GLN A 597      31.401  17.246  66.482  1.00  0.00
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ATOM	662	CB	GLN	A	597	31.509	18.709	66.071	1.00	0.00
ATOM	663	CG	GLN	A	597	30.300	19.504	66.547	1.00	0.00
ATOM	664	CD	GLN	A	597	30.469	20.978	66.197	1.00	0.00
ATOM	665	OE1	GLN	A	597	31.241	21.709	66.833	1.00	0.00
ATOM	666	NE2	GLN	A	597	29.741	21.399	65.177	1.00	0.00
ATOM	669	C	GLN	A	597	32.514	16.446	65.808	1.00	0.00
ATOM	670	O	GLN	A	597	32.279	15.884	64.735	1.00	0.00
ATOM	671	N	TYR	A	598	33.628	16.229	66.483	1.00	0.00
ATOM	673	CA	TYR	A	598	34.695	15.440	65.861	1.00	0.00
ATOM	674	CB	TYR	A	598	36.050	15.808	66.465	1.00	0.00
ATOM	675	CG	TYR	A	598	36.616	17.205	66.194	1.00	0.00
ATOM	676	CD1	TYR	A	598	35.993	18.095	65.326	1.00	0.00
ATOM	677	CE1	TYR	A	598	36.538	19.353	65.107	1.00	0.00
ATOM	678	CZ	TYR	A	598	37.709	19.718	65.755	1.00	0.00
ATOM	679	OH	TYR	A	598	38.266	20.957	65.529	1.00	0.00
ATOM	680	CE2	TYR	A	598	38.333	18.834	66.622	1.00	0.00
ATOM	681	CD2	TYR	A	598	37.786	17.578	66.841	1.00	0.00
ATOM	682	C	TYR	A	598	34.467	13.954	66.103	1.00	0.00
ATOM	683	O	TYR	A	598	34.723	13.121	65.224	1.00	0.00
ATOM	684	N	SER	A	599	33.841	13.653	67.227	1.00	0.00
ATOM	686	CA	SER	A	599	33.624	12.259	67.620	1.00	0.00
ATOM	687	CB	SER	A	599	33.723	12.174	69.136	1.00	0.00
ATOM	688	OG	SER	A	599	32.627	12.901	69.675	1.00	0.00
ATOM	689	C	SER	A	599	32.271	11.690	67.204	1.00	0.00
ATOM	690	O	SER	A	599	32.081	10.475	67.351	1.00	0.00
ATOM	691	N	TRP	A	600	31.435	12.468	66.531	1.00	0.00
ATOM	693	CA	TRP	A	600	30.040	12.049	66.305	1.00	0.00
ATOM	694	CB	TRP	A	600	29.232	13.214	65.714	1.00	0.00
ATOM	695	CG	TRP	A	600	29.398	13.482	64.224	1.00	0.00
ATOM	696	CD1	TRP	A	600	30.539	13.900	63.574	1.00	0.00
ATOM	697	NE1	TRP	A	600	30.273	14.004	62.250	1.00	0.00
ATOM	699	CE2	TRP	A	600	28.996	13.673	61.983	1.00	0.00
ATOM	700	CZ2	TRP	A	600	28.262	13.629	60.808	1.00	0.00
ATOM	701	CH2	TRP	A	600	26.927	13.240	60.843	1.00	0.00
ATOM	702	CZ3	TRP	A	600	26.327	12.899	62.052	1.00	0.00
ATOM	703	CE3	TRP	A	600	27.054	12.944	63.234	1.00	0.00
ATOM	704	CD2	TRP	A	600	28.386	13.332	63.204	1.00	0.00
ATOM	705	C	TRP	A	600	29.909	10.820	65.402	1.00	0.00
ATOM	706	O	TRP	A	600	29.151	9.910	65.763	1.00	0.00
ATOM	707	N	MET	A	601	30.850	10.632	64.487	1.00	0.00
ATOM	709	CA	MET	A	601	30.744	9.511	63.559	1.00	0.00
ATOM	710	CB	MET	A	601	31.575	9.809	62.319	1.00	0.00
ATOM	711	CG	MET	A	601	30.690	9.840	61.079	1.00	0.00
ATOM	712	SD	MET	A	601	29.759	8.325	60.753	1.00	0.00

ATOM	713	CE	MET	A	601	28.886	8.842	59.258	1.00	0.00
ATOM	714	C	MET	A	601	31.206	8.206	64.187	1.00	0.00
ATOM	715	O	MET	A	601	30.581	7.168	63.946	1.00	0.00
ATOM	716	N	PHE	A	602	32.096	8.276	65.162	1.00	0.00
ATOM	718	CA	PHE	A	602	32.505	7.022	65.779	1.00	0.00
ATOM	719	CB	PHE	A	602	33.998	6.996	66.065	1.00	0.00
ATOM	720	CG	PHE	A	602	34.476	5.568	66.316	1.00	0.00
ATOM	721	CD1	PHE	A	602	33.801	4.508	65.720	1.00	0.00
ATOM	722	CE1	PHE	A	602	34.205	3.202	65.957	1.00	0.00
ATOM	723	CZ	PHE	A	602	35.293	2.956	66.780	1.00	0.00
ATOM	724	CE2	PHE	A	602	35.988	4.014	67.350	1.00	0.00
ATOM	725	CD2	PHE	A	602	35.583	5.322	67.114	1.00	0.00
ATOM	726	C	PHE	A	602	31.693	6.751	67.040	1.00	0.00
ATOM	727	O	PHE	A	602	31.553	5.587	67.425	1.00	0.00
ATOM	728	N	LEU	A	603	30.974	7.744	67.531	1.00	0.00
ATOM	730	CA	LEU	A	603	30.038	7.458	68.617	1.00	0.00
ATOM	731	CB	LEU	A	603	29.579	8.757	69.271	1.00	0.00
ATOM	732	CG	LEU	A	603	30.709	9.450	70.024	1.00	0.00
ATOM	733	CD1	LEU	A	603	30.235	10.779	70.601	1.00	0.00
ATOM	734	CD2	LEU	A	603	31.272	8.559	71.126	1.00	0.00
ATOM	735	C	LEU	A	603	28.837	6.696	68.069	1.00	0.00
ATOM	736	O	LEU	A	603	28.516	5.617	68.589	1.00	0.00
ATOM	737	N	MET	A	604	28.399	7.068	66.876	1.00	0.00
ATOM	739	CA	MET	A	604	27.269	6.355	66.278	1.00	0.00
ATOM	740	CB	MET	A	604	26.546	7.278	65.295	1.00	0.00
ATOM	741	CG	MET	A	604	27.430	7.788	64.164	1.00	0.00
ATOM	742	SD	MET	A	604	26.649	8.960	63.033	1.00	0.00
ATOM	743	CE	MET	A	604	25.297	7.919	62.439	1.00	0.00
ATOM	744	C	MET	A	604	27.687	5.039	65.612	1.00	0.00
ATOM	745	O	MET	A	604	26.922	4.069	65.699	1.00	0.00
ATOM	746	N	ALA	A	605	28.948	4.916	65.223	1.00	0.00
ATOM	748	CA	ALA	A	605	29.417	3.659	64.631	1.00	0.00
ATOM	749	CB	ALA	A	605	30.571	3.954	63.682	1.00	0.00
ATOM	750	C	ALA	A	605	29.864	2.639	65.675	1.00	0.00
ATOM	751	O	ALA	A	605	29.707	1.434	65.448	1.00	0.00
ATOM	752	N	PHE	A	606	30.208	3.099	66.867	1.00	0.00
ATOM	754	CA	PHE	A	606	30.563	2.168	67.938	1.00	0.00
ATOM	755	CB	PHE	A	606	31.488	2.877	68.920	1.00	0.00
ATOM	756	CG	PHE	A	606	32.423	1.957	69.697	1.00	0.00
ATOM	757	CD1	PHE	A	606	32.882	0.782	69.115	1.00	0.00
ATOM	758	CE1	PHE	A	606	33.747	-0.048	69.816	1.00	0.00
ATOM	759	CZ	PHE	A	606	34.155	0.297	71.098	1.00	0.00
ATOM	760	CE2	PHE	A	606	33.697	1.472	71.680	1.00	0.00
ATOM	761	CD2	PHE	A	606	32.830	2.300	70.980	1.00	0.00

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ATOM    762  C   PHE A 606      29.292   1.717  68.645  1.00  0.00
ATOM    763  O   PHE A 606      29.201   0.564  69.090  1.00  0.00
ATOM    764  N   ALA A 607      28.256   2.536  68.531  1.00  0.00
ATOM    766  CA  ALA A 607      26.931   2.134  68.999  1.00  0.00
ATOM    767  CB  ALA A 607      26.015   3.353  69.019  1.00  0.00
ATOM    768  C   ALA A 607      26.358   1.075  68.068  1.00  0.00
ATOM    769  O   ALA A 607      25.956   0.011  68.549  1.00  0.00
ATOM    770  N   LEU A 608      26.588   1.243  66.774  1.00  0.00
ATOM    772  CA  LEU A 608      26.178   0.243  65.778  1.00  0.00
ATOM    773  CB  LEU A 608      26.480   0.825  64.402  1.00  0.00
ATOM    774  CG  LEU A 608      26.293  -0.194  63.284  1.00  0.00
ATOM    775  CD1 LEU A 608      24.846  -0.648  63.180  1.00  0.00
ATOM    776  CD2 LEU A 608      26.758   0.383  61.957  1.00  0.00
ATOM    777  C   LEU A 608      26.943  -1.067  65.949  1.00  0.00
ATOM    778  O   LEU A 608      26.328  -2.141  65.989  1.00  0.00
ATOM    779  N   GLY A 609      28.229  -0.952  66.243  1.00  0.00
ATOM    781  CA  GLY A 609      29.068  -2.113  66.542  1.00  0.00
ATOM    782  C   GLY A 609      28.504  -2.934  67.694  1.00  0.00
ATOM    783  O   GLY A 609      28.122  -4.094  67.488  1.00  0.00
ATOM    784  N   TRP A 610      28.237  -2.271  68.808  1.00  0.00
ATOM    786  CA  TRP A 610      27.778  -2.964  70.012  1.00  0.00
ATOM    787  CB  TRP A 610      27.928  -1.998  71.173  1.00  0.00
ATOM    788  CG  TRP A 610      27.755  -2.641  72.528  1.00  0.00
ATOM    789  CD1 TRP A 610      26.658  -2.568  73.358  1.00  0.00
ATOM    790  NE1 TRP A 610      26.925  -3.278  74.483  1.00  0.00
ATOM    792  CE2 TRP A 610      28.158  -3.820  74.436  1.00  0.00
ATOM    793  CZ2 TRP A 610      28.880  -4.593  75.328  1.00  0.00
ATOM    794  CH2 TRP A 610      30.164  -5.012  74.995  1.00  0.00
ATOM    795  CZ3 TRP A 610      30.726  -4.656  73.774  1.00  0.00
ATOM    796  CE3 TRP A 610      30.011  -3.878  72.876  1.00  0.00
ATOM    797  CD2 TRP A 610      28.730  -3.457  73.206  1.00  0.00
ATOM    798  C   TRP A 610      26.323  -3.424  69.949  1.00  0.00
ATOM    799  O   TRP A 610      26.014  -4.495  70.485  1.00  0.00
ATOM    800  N   ARG A 611      25.492  -2.762  69.162  1.00  0.00
ATOM    802  CA  ARG A 611      24.107  -3.219  69.027  1.00  0.00
ATOM    803  CB  ARG A 611      23.235  -2.083  68.512  1.00  0.00
ATOM    804  CG  ARG A 611      23.117  -0.950  69.523  1.00  0.00
ATOM    805  CD  ARG A 611      22.226   0.158  68.981  1.00  0.00
ATOM    806  NE  ARG A 611      22.725   0.624  67.678  1.00  0.00
ATOM    807  CZ  ARG A 611      22.559   1.868  67.227  1.00  0.00
ATOM    808  NH1 ARG A 611      21.888   2.760  67.961  1.00  0.00
ATOM    809  NH2 ARG A 611      23.050   2.216  66.036  1.00  0.00
ATOM    810  C   ARG A 611      24.014  -4.402  68.074  1.00  0.00
ATOM    811  O   ARG A 611      23.218  -5.317  68.315  1.00  0.00
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ATOM    812  N   SER A 612      24.963  -4.499  67.159  1.00  0.00
ATOM    814  CA  SER A 612      25.031  -5.671  66.291  1.00  0.00
ATOM    815  CB  SER A 612      25.949  -5.357  65.123  1.00  0.00
ATOM    816  OG  SER A 612      25.359  -4.282  64.414  1.00  0.00
ATOM    817  C   SER A 612      25.595  -6.845  67.066  1.00  0.00
ATOM    818  O   SER A 612      24.998  -7.932  67.061  1.00  0.00
ATOM    819  N   TYR A 613      26.556  -6.544  67.924  1.00  0.00
ATOM    821  CA  TYR A 613      27.149  -7.554  68.799  1.00  0.00
ATOM    822  CB  TYR A 613      28.266  -6.892  69.600  1.00  0.00
ATOM    823  CG  TYR A 613      29.046  -7.820  70.528  1.00  0.00
ATOM    824  CD1 TYR A 613      29.154  -9.176  70.243  1.00  0.00
ATOM    825  CE1 TYR A 613      29.872 -10.007  71.092  1.00  0.00
ATOM    826  CZ  TYR A 613      30.487  -9.480  72.219  1.00  0.00
ATOM    827  OH  TYR A 613      31.350 -10.262  72.951  1.00  0.00
ATOM    828  CE2 TYR A 613      30.369  -8.129  72.513  1.00  0.00
ATOM    829  CD2 TYR A 613      29.646  -7.300  71.667  1.00  0.00
ATOM    830  C   TYR A 613      26.098  -8.149  69.732  1.00  0.00
ATOM    831  O   TYR A 613      25.861  -9.360  69.661  1.00  0.00
ATOM    832  N   ARG A 614      25.301  -7.297  70.352  1.00  0.00
ATOM    834  CA  ARG A 614      24.261  -7.779  71.260  1.00  0.00
ATOM    835  CB  ARG A 614      23.755  -6.602  72.083  1.00  0.00
ATOM    836  CG  ARG A 614      24.793  -6.158  73.104  1.00  0.00
ATOM    837  CD  ARG A 614      25.104  -7.292  74.075  1.00  0.00
ATOM    838  NE  ARG A 614      26.038  -6.865  75.129  1.00  0.00
ATOM    839  CZ  ARG A 614      25.667  -6.698  76.401  1.00  0.00
ATOM    840  NH1 ARG A 614      24.396  -6.898  76.758  1.00  0.00
ATOM    841  NH2 ARG A 614      26.563  -6.319  77.315  1.00  0.00
ATOM    842  C   ARG A 614      23.083  -8.445  70.553  1.00  0.00
ATOM    843  O   ARG A 614      22.912  -9.662  70.685  1.00  0.00
ATOM    844  N   GLN A 615      22.409  -7.721  69.674  1.00  0.00
ATOM    846  CA  GLN A 615      21.115  -8.198  69.168  1.00  0.00
ATOM    847  CB  GLN A 615      20.284  -6.973  68.777  1.00  0.00
ATOM    848  CG  GLN A 615      18.816  -7.326  68.538  1.00  0.00
ATOM    849  CD  GLN A 615      17.992  -6.089  68.185  1.00  0.00
ATOM    850  OE1 GLN A 615      18.283  -4.972  68.631  1.00  0.00
ATOM    851  NE2 GLN A 615      16.941  -6.320  67.419  1.00  0.00
ATOM    854  C   GLN A 615      21.214  -9.180  67.993  1.00  0.00
ATOM    855  O   GLN A 615      20.241  -9.893  67.722  1.00  0.00
ATOM    856  N   SER A 616      22.363  -9.283  67.345  1.00  0.00
ATOM    858  CA  SER A 616      22.472 -10.273  66.267  1.00  0.00
ATOM    859  CB  SER A 616      22.640  -9.570  64.925  1.00  0.00
ATOM    860  OG  SER A 616      24.018  -9.260  64.758  1.00  0.00
ATOM    861  C   SER A 616      23.648 -11.225  66.457  1.00  0.00
ATOM    862  O   SER A 616      23.869 -12.079  65.593  1.00  0.00
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ATOM    863  N   SER A 617      24.401 -11.069  67.537  1.00  0.00
ATOM    865  CA  SER A 617      25.662 -11.813  67.737  1.00  0.00
ATOM    866  CB  SER A 617      25.405 -13.317  67.801  1.00  0.00
ATOM    867  OG  SER A 617      26.636 -13.965  68.091  1.00  0.00
ATOM    868  C   SER A 617      26.655 -11.458  66.629  1.00  0.00
ATOM    869  O   SER A 617      27.124 -12.313  65.866  1.00  0.00
ATOM    870  N   ALA A 618      26.799 -10.151  66.470  1.00  0.00
ATOM    872  CA  ALA A 618      27.716  -9.457  65.542  1.00  0.00
ATOM    873  CB  ALA A 618      29.126  -9.555  66.103  1.00  0.00
ATOM    874  C   ALA A 618      27.743  -9.869  64.067  1.00  0.00
ATOM    875  O   ALA A 618      28.769  -9.651  63.412  1.00  0.00
ATOM    876  N   ASN A 619      26.663 -10.413  63.531  1.00  0.00
ATOM    878  CA  ASN A 619      26.655 -10.707  62.098  1.00  0.00
ATOM    879  CB  ASN A 619      26.274 -12.171  61.876  1.00  0.00
ATOM    880  CG  ASN A 619      25.046 -12.570  62.689  1.00  0.00
ATOM    881  OD1 ASN A 619      23.958 -12.001  62.539  1.00  0.00
ATOM    882  ND2 ASN A 619      25.238 -13.565  63.536  1.00  0.00
ATOM    885  C   ASN A 619      25.759  -9.779  61.276  1.00  0.00
ATOM    886  O   ASN A 619      25.995  -9.640  60.070  1.00  0.00
ATOM    887  N   LEU A 620      24.789  -9.111  61.885  1.00  0.00
ATOM    889  CA  LEU A 620      23.941  -8.201  61.109  1.00  0.00
ATOM    890  CB  LEU A 620      22.482  -8.648  61.178  1.00  0.00
ATOM    891  CG  LEU A 620      22.267 -10.064  60.651  1.00  0.00
ATOM    892  CD1 LEU A 620      20.812 -10.490  60.813  1.00  0.00
ATOM    893  CD2 LEU A 620      22.709 -10.203  59.198  1.00  0.00
ATOM    894  C   LEU A 620      24.061  -6.803  61.686  1.00  0.00
ATOM    895  O   LEU A 620      24.332  -6.640  62.882  1.00  0.00
ATOM    896  N   LEU A 621      23.840  -5.806  60.848  1.00  0.00
ATOM    898  CA  LEU A 621      23.954  -4.420  61.305  1.00  0.00
ATOM    899  CB  LEU A 621      24.308  -3.512  60.139  1.00  0.00
ATOM    900  CG  LEU A 621      25.760  -3.705  59.726  1.00  0.00
ATOM    901  CD1 LEU A 621      26.101  -2.813  58.543  1.00  0.00
ATOM    902  CD2 LEU A 621      26.699  -3.420  60.895  1.00  0.00
ATOM    903  C   LEU A 621      22.681  -3.941  61.984  1.00  0.00
ATOM    904  O   LEU A 621      21.679  -3.588  61.349  1.00  0.00
ATOM    905  N   CYS A 622      22.786  -3.844  63.293  1.00  0.00
ATOM    907  CA  CYS A 622      21.660  -3.399  64.108  1.00  0.00
ATOM    908  CB  CYS A 622      21.679  -4.108  65.452  1.00  0.00
ATOM    909  SG  CYS A 622      20.424  -3.549  66.627  1.00  0.00
ATOM    910  C   CYS A 622      21.738  -1.900  64.321  1.00  0.00
ATOM    911  O   CYS A 622      22.496  -1.408  65.164  1.00  0.00
ATOM    912  N   PHE A 623      20.958  -1.181  63.533  1.00  0.00
ATOM    914  CA  PHE A 623      20.917   0.275  63.655  1.00  0.00
ATOM    915  CB  PHE A 623      20.624   0.882  62.287  1.00  0.00
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ATOM    916  CG  PHE A 623      21.739   0.764  61.252  1.00  0.00
ATOM    917  CD1 PHE A 623      22.768   1.697  61.241  1.00  0.00
ATOM    918  CE1 PHE A 623      23.780   1.604  60.295  1.00  0.00
ATOM    919  CZ  PHE A 623      23.763   0.580  59.357  1.00  0.00
ATOM    920  CE2 PHE A 623      22.733  -0.350  59.366  1.00  0.00
ATOM    921  CD2 PHE A 623      21.720  -0.257  60.311  1.00  0.00
ATOM    922  C   PHE A 623      19.809   0.658  64.622  1.00  0.00
ATOM    923  O   PHE A 623      19.852   1.699  65.286  1.00  0.00
ATOM    924  N   ALA A 624      18.868  -0.256  64.749  1.00  0.00
ATOM    926  CA  ALA A 624      17.746  -0.077  65.665  1.00  0.00
ATOM    927  CB  ALA A 624      16.787   0.909  65.009  1.00  0.00
ATOM    928  C   ALA A 624      17.065  -1.423  65.853  1.00  0.00
ATOM    929  O   ALA A 624      17.204  -2.292  64.984  1.00  0.00
ATOM    930  N   PRO A 625      16.223  -1.562  66.867  1.00  0.00
ATOM    931  CA  PRO A 625      15.400  -2.777  66.970  1.00  0.00
ATOM    932  CB  PRO A 625      14.682  -2.644  68.279  1.00  0.00
ATOM    933  CG  PRO A 625      14.985  -1.282  68.887  1.00  0.00
ATOM    934  CD  PRO A 625      15.945  -0.593  67.932  1.00  0.00
ATOM    935  C   PRO A 625      14.407  -2.928  65.803  1.00  0.00
ATOM    936  O   PRO A 625      14.127  -4.055  65.379  1.00  0.00
ATOM    937  N   ASP A 626      14.030  -1.813  65.189  1.00  0.00
ATOM    939  CA  ASP A 626      13.174  -1.813  63.994  1.00  0.00
ATOM    940  CB  ASP A 626      12.237  -0.598  64.034  1.00  0.00
ATOM    941  CG  ASP A 626      12.982   0.736  63.929  1.00  0.00
ATOM    942  OD1 ASP A 626      13.627   1.110  64.901  1.00  0.00
ATOM    943  OD2 ASP A 626      12.763   1.458  62.963  1.00  0.00
ATOM    944  C   ASP A 626      13.974  -1.790  62.686  1.00  0.00
ATOM    945  O   ASP A 626      13.374  -1.775  61.605  1.00  0.00
ATOM    946  N   LEU A 627      15.297  -1.811  62.774  1.00  0.00
ATOM    948  CA  LEU A 627      16.135  -1.725  61.571  1.00  0.00
ATOM    949  CB  LEU A 627      16.541  -0.272  61.354  1.00  0.00
ATOM    950  CG  LEU A 627      17.229  -0.082  60.006  1.00  0.00
ATOM    951  CD1 LEU A 627      16.321  -0.525  58.863  1.00  0.00
ATOM    952  CD2 LEU A 627      17.659   1.367  59.815  1.00  0.00
ATOM    953  C   LEU A 627      17.379  -2.609  61.697  1.00  0.00
ATOM    954  O   LEU A 627      18.441  -2.175  62.175  1.00  0.00
ATOM    955  N   ILE A 628      17.212  -3.854  61.282  1.00  0.00
ATOM    957  CA  ILE A 628      18.310  -4.831  61.278  1.00  0.00
ATOM    958  CB  ILE A 628      17.836  -6.121  61.943  1.00  0.00
ATOM    959  CG2 ILE A 628      18.979  -7.131  62.016  1.00  0.00
ATOM    960  CG1 ILE A 628      17.292  -5.862  63.342  1.00  0.00
ATOM    961  CD1 ILE A 628      18.399  -5.394  64.274  1.00  0.00
ATOM    962  C   ILE A 628      18.721  -5.133  59.841  1.00  0.00
ATOM    963  O   ILE A 628      18.089  -5.945  59.150  1.00  0.00
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ATOM	964	N	ILE	A	629	19.800	-4.504	59.417	1.00	0.00
ATOM	966	CA	ILE	A	629	20.255	-4.648	58.035	1.00	0.00
ATOM	967	CB	ILE	A	629	21.033	-3.398	57.642	1.00	0.00
ATOM	968	CG2	ILE	A	629	21.708	-3.589	56.288	1.00	0.00
ATOM	969	CG1	ILE	A	629	20.113	-2.184	57.608	1.00	0.00
ATOM	970	CD1	ILE	A	629	19.048	-2.326	56.527	1.00	0.00
ATOM	971	C	ILE	A	629	21.113	-5.891	57.843	1.00	0.00
ATOM	972	O	ILE	A	629	22.222	-6.019	58.379	1.00	0.00
ATOM	973	N	ASN	A	630	20.530	-6.847	57.143	1.00	0.00
ATOM	975	CA	ASN	A	630	21.286	-8.016	56.703	1.00	0.00
ATOM	976	CB	ASN	A	630	20.371	-9.236	56.584	1.00	0.00
ATOM	977	CG	ASN	A	630	19.231	-9.020	55.595	1.00	0.00
ATOM	978	OD1	ASN	A	630	19.454	-8.971	54.379	1.00	0.00
ATOM	979	ND2	ASN	A	630	18.016	-9.001	56.117	1.00	0.00
ATOM	982	C	ASN	A	630	21.984	-7.690	55.387	1.00	0.00
ATOM	983	O	ASN	A	630	21.666	-6.685	54.735	1.00	0.00
ATOM	984	N	GLU	A	631	22.800	-8.618	54.919	1.00	0.00
ATOM	986	CA	GLU	A	631	23.664	-8.354	53.757	1.00	0.00
ATOM	987	CB	GLU	A	631	24.838	-9.345	53.721	1.00	0.00
ATOM	988	CG	GLU	A	631	24.486	-10.782	53.317	1.00	0.00
ATOM	989	CD	GLU	A	631	24.159	-11.676	54.514	1.00	0.00
ATOM	990	OE1	GLU	A	631	25.048	-12.398	54.937	1.00	0.00
ATOM	991	OE2	GLU	A	631	23.111	-11.453	55.121	1.00	0.00
ATOM	992	C	GLU	A	631	22.919	-8.369	52.414	1.00	0.00
ATOM	993	O	GLU	A	631	23.433	-7.814	51.438	1.00	0.00
ATOM	994	N	GLN	A	632	21.658	-8.773	52.419	1.00	0.00
ATOM	996	CA	GLN	A	632	20.849	-8.769	51.199	1.00	0.00
ATOM	997	CB	GLN	A	632	19.841	-9.923	51.219	1.00	0.00
ATOM	998	CG	GLN	A	632	20.456	-11.308	50.997	1.00	0.00
ATOM	999	CD	GLN	A	632	20.990	-11.938	52.284	1.00	0.00
ATOM	1000	OE1	GLN	A	632	22.124	-12.427	52.327	1.00	0.00
ATOM	1001	NE2	GLN	A	632	20.203	-11.842	53.342	1.00	0.00
ATOM	1004	C	GLN	A	632	20.083	-7.455	51.042	1.00	0.00
ATOM	1005	O	GLN	A	632	19.446	-7.237	50.005	1.00	0.00
ATOM	1006	N	ARG	A	633	20.146	-6.586	52.041	1.00	0.00
ATOM	1008	CA	ARG	A	633	19.444	-5.304	51.928	1.00	0.00
ATOM	1009	CB	ARG	A	633	18.962	-4.865	53.303	1.00	0.00
ATOM	1010	CG	ARG	A	633	18.282	-6.014	54.029	1.00	0.00
ATOM	1011	CD	ARG	A	633	17.471	-5.518	55.213	1.00	0.00
ATOM	1012	NE	ARG	A	633	16.273	-4.832	54.715	1.00	0.00
ATOM	1013	CZ	ARG	A	633	15.417	-4.165	55.490	1.00	0.00
ATOM	1014	NH1	ARG	A	633	15.680	-3.992	56.788	1.00	0.00
ATOM	1015	NH2	ARG	A	633	14.332	-3.614	54.946	1.00	0.00
ATOM	1016	C	ARG	A	633	20.350	-4.223	51.358	1.00	0.00

ATOM	1017	O	ARG	A	633	19.866	-3.225	50.808	1.00	0.00
ATOM	1018	N	MET	A	634	21.649	-4.463	51.388	1.00	0.00
ATOM	1020	CA	MET	A	634	22.582	-3.481	50.832	1.00	0.00
ATOM	1021	CB	MET	A	634	23.781	-3.338	51.755	1.00	0.00
ATOM	1022	CG	MET	A	634	23.365	-2.639	53.042	1.00	0.00
ATOM	1023	SD	MET	A	634	22.588	-1.024	52.799	1.00	0.00
ATOM	1024	CE	MET	A	634	22.391	-0.515	54.522	1.00	0.00
ATOM	1025	C	MET	A	634	23.013	-3.864	49.424	1.00	0.00
ATOM	1026	O	MET	A	634	24.138	-4.318	49.189	1.00	0.00
ATOM	1027	N	THR	A	635	22.134	-3.554	48.485	1.00	0.00
ATOM	1029	CA	THR	A	635	22.369	-3.888	47.078	1.00	0.00
ATOM	1030	CB	THR	A	635	21.008	-4.091	46.411	1.00	0.00
ATOM	1031	OG1	THR	A	635	21.211	-4.321	45.024	1.00	0.00
ATOM	1032	CG2	THR	A	635	20.096	-2.877	46.566	1.00	0.00
ATOM	1033	C	THR	A	635	23.194	-2.824	46.345	1.00	0.00
ATOM	1034	O	THR	A	635	23.726	-3.090	45.261	1.00	0.00
ATOM	1035	N	LEU	A	636	23.365	-1.664	46.958	1.00	0.00
ATOM	1037	CA	LEU	A	636	24.251	-0.649	46.383	1.00	0.00
ATOM	1038	CB	LEU	A	636	23.785	0.731	46.860	1.00	0.00
ATOM	1039	CG	LEU	A	636	24.373	1.897	46.057	1.00	0.00
ATOM	1040	CD1	LEU	A	636	23.423	3.086	46.029	1.00	0.00
ATOM	1041	CD2	LEU	A	636	25.753	2.332	46.541	1.00	0.00
ATOM	1042	C	LEU	A	636	25.670	-0.967	46.844	1.00	0.00
ATOM	1043	O	LEU	A	636	25.964	-0.877	48.042	1.00	0.00
ATOM	1044	N	PRO	A	637	26.561	-1.189	45.889	1.00	0.00
ATOM	1045	CA	PRO	A	637	27.835	-1.858	46.181	1.00	0.00
ATOM	1046	CB	PRO	A	637	28.485	-2.063	44.846	1.00	0.00
ATOM	1047	CG	PRO	A	637	27.568	-1.545	43.748	1.00	0.00
ATOM	1048	CD	PRO	A	637	26.323	-1.032	44.450	1.00	0.00
ATOM	1049	C	PRO	A	637	28.749	-1.069	47.119	1.00	0.00
ATOM	1050	O	PRO	A	637	29.155	-1.622	48.146	1.00	0.00
ATOM	1051	N	CYS	A	638	28.778	0.247	46.973	1.00	0.00
ATOM	1053	CA	CYS	A	638	29.640	1.074	47.829	1.00	0.00
ATOM	1054	CB	CYS	A	638	29.791	2.441	47.175	1.00	0.00
ATOM	1055	SG	CYS	A	638	30.496	2.427	45.511	1.00	0.00
ATOM	1056	C	CYS	A	638	29.076	1.242	49.241	1.00	0.00
ATOM	1057	O	CYS	A	638	29.847	1.199	50.209	1.00	0.00
ATOM	1058	N	MET	A	639	27.769	1.080	49.370	1.00	0.00
ATOM	1060	CA	MET	A	639	27.129	1.175	50.677	1.00	0.00
ATOM	1061	CB	MET	A	639	25.646	1.457	50.467	1.00	0.00
ATOM	1062	CG	MET	A	639	24.918	1.641	51.792	1.00	0.00
ATOM	1063	SD	MET	A	639	25.516	2.998	52.822	1.00	0.00
ATOM	1064	CE	MET	A	639	24.392	2.809	54.225	1.00	0.00
ATOM	1065	C	MET	A	639	27.313	-0.136	51.428	1.00	0.00

ATOM	1066	O	MET	A	639	27.702	-0.104	52.601	1.00	0.00
ATOM	1067	N	TYR	A	640	27.376	-1.226	50.678	1.00	0.00
ATOM	1069	CA	TYR	A	640	27.632	-2.544	51.264	1.00	0.00
ATOM	1070	CB	TYR	A	640	27.194	-3.604	50.263	1.00	0.00
ATOM	1071	CG	TYR	A	640	27.344	-5.031	50.776	1.00	0.00
ATOM	1072	CD1	TYR	A	640	26.853	-5.370	52.031	1.00	0.00
ATOM	1073	CE1	TYR	A	640	26.992	-6.668	52.503	1.00	0.00
ATOM	1074	CZ	TYR	A	640	27.620	-7.624	51.716	1.00	0.00
ATOM	1075	OH	TYR	A	640	27.774	-8.907	52.191	1.00	0.00
ATOM	1076	CE2	TYR	A	640	28.107	-7.290	50.460	1.00	0.00
ATOM	1077	CD2	TYR	A	640	27.968	-5.991	49.989	1.00	0.00
ATOM	1078	C	TYR	A	640	29.114	-2.737	51.587	1.00	0.00
ATOM	1079	O	TYR	A	640	29.441	-3.369	52.598	1.00	0.00
ATOM	1080	N	ASP	A	641	29.970	-1.993	50.906	1.00	0.00
ATOM	1082	CA	ASP	A	641	31.403	-2.022	51.212	1.00	0.00
ATOM	1083	CB	ASP	A	641	32.174	-1.359	50.073	1.00	0.00
ATOM	1084	CG	ASP	A	641	31.985	-2.107	48.754	1.00	0.00
ATOM	1085	OD1	ASP	A	641	31.899	-3.328	48.792	1.00	0.00
ATOM	1086	OD2	ASP	A	641	32.034	-1.450	47.721	1.00	0.00
ATOM	1087	C	ASP	A	641	31.680	-1.266	52.507	1.00	0.00
ATOM	1088	O	ASP	A	641	32.427	-1.759	53.361	1.00	0.00
ATOM	1089	N	GLN	A	642	30.885	-0.239	52.763	1.00	0.00
ATOM	1091	CA	GLN	A	642	30.995	0.486	54.028	1.00	0.00
ATOM	1092	CB	GLN	A	642	30.375	1.863	53.850	1.00	0.00
ATOM	1093	CG	GLN	A	642	30.481	2.664	55.138	1.00	0.00
ATOM	1094	CD	GLN	A	642	29.900	4.054	54.938	1.00	0.00
ATOM	1095	OE1	GLN	A	642	30.613	5.055	55.070	1.00	0.00
ATOM	1096	NE2	GLN	A	642	28.615	4.098	54.636	1.00	0.00
ATOM	1099	C	GLN	A	642	30.292	-0.260	55.162	1.00	0.00
ATOM	1100	O	GLN	A	642	30.757	-0.219	56.308	1.00	0.00
ATOM	1101	N	CYS	A	643	29.367	-1.135	54.805	1.00	0.00
ATOM	1103	CA	CYS	A	643	28.738	-2.009	55.795	1.00	0.00
ATOM	1104	CB	CYS	A	643	27.440	-2.559	55.219	1.00	0.00
ATOM	1105	SG	CYS	A	643	26.127	-1.339	54.997	1.00	0.00
ATOM	1106	C	CYS	A	643	29.655	-3.156	56.201	1.00	0.00
ATOM	1107	O	CYS	A	643	29.618	-3.566	57.365	1.00	0.00
ATOM	1108	N	LYS	A	644	30.634	-3.471	55.367	1.00	0.00
ATOM	1110	CA	LYS	A	644	31.654	-4.447	55.759	1.00	0.00
ATOM	1111	CB	LYS	A	644	32.305	-5.027	54.507	1.00	0.00
ATOM	1112	CG	LYS	A	644	31.338	-5.789	53.595	1.00	0.00
ATOM	1113	CD	LYS	A	644	30.873	-7.138	54.153	1.00	0.00
ATOM	1114	CE	LYS	A	644	29.694	-7.035	55.121	1.00	0.00
ATOM	1115	NZ	LYS	A	644	29.317	-8.358	55.640	1.00	0.00
ATOM	1116	C	LYS	A	644	32.715	-3.800	56.645	1.00	0.00

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ATOM   1117  O   LYS A 644      33.216  -4.451  57.568  1.00  0.00
ATOM   1118  N   HIS A 645      32.825  -2.484  56.555  1.00  0.00
ATOM   1120  CA  HIS A 645      33.718  -1.738  57.445  1.00  0.00
ATOM   1121  CB  HIS A 645      33.965  -0.352  56.860  1.00  0.00
ATOM   1122  CG  HIS A 645      35.017  -0.284  55.773  1.00  0.00
ATOM   1123  ND1 HIS A 645      34.846  -0.527  54.460  1.00  0.00
ATOM   1125  CE1 HIS A 645      36.020  -0.349  53.819  1.00  0.00
ATOM   1126  NE2 HIS A 645      36.942   0.002  54.743  1.00  0.00
ATOM   1127  CD2 HIS A 645      36.341   0.042  55.952  1.00  0.00
ATOM   1128  C   HIS A 645      33.109  -1.592  58.835  1.00  0.00
ATOM   1129  O   HIS A 645      33.808  -1.785  59.837  1.00  0.00
ATOM   1130  N   MET A 646      31.790  -1.510  58.889  1.00  0.00
ATOM   1132  CA  MET A 646      31.101  -1.452  60.182  1.00  0.00
ATOM   1133  CB  MET A 646      29.788  -0.706  59.981  1.00  0.00
ATOM   1134  CG  MET A 646      30.071   0.699  59.456  1.00  0.00
ATOM   1135  SD  MET A 646      28.641   1.774  59.196  1.00  0.00
ATOM   1136  CE  MET A 646      27.754   0.800  57.960  1.00  0.00
ATOM   1137  C   MET A 646      30.871  -2.850  60.763  1.00  0.00
ATOM   1138  O   MET A 646      30.815  -3.016  61.990  1.00  0.00
ATOM   1139  N   LEU A 647      31.021  -3.852  59.910  1.00  0.00
ATOM   1141  CA  LEU A 647      31.002  -5.246  60.351  1.00  0.00
ATOM   1142  CB  LEU A 647      30.748  -6.136  59.136  1.00  0.00
ATOM   1143  CG  LEU A 647      29.661  -7.185  59.372  1.00  0.00
ATOM   1144  CD1 LEU A 647      30.022  -8.157  60.490  1.00  0.00
ATOM   1145  CD2 LEU A 647      28.310  -6.535  59.645  1.00  0.00
ATOM   1146  C   LEU A 647      32.347  -5.613  60.976  1.00  0.00
ATOM   1147  O   LEU A 647      32.373  -6.428  61.904  1.00  0.00
ATOM   1148  N   TYR A 648      33.385  -4.847  60.671  1.00  0.00
ATOM   1150  CA  TYR A 648      34.680  -5.063  61.324  1.00  0.00
ATOM   1151  CB  TYR A 648      35.785  -4.317  60.579  1.00  0.00
ATOM   1152  CG  TYR A 648      36.029  -4.744  59.134  1.00  0.00
ATOM   1153  CD1 TYR A 648      36.440  -3.796  58.205  1.00  0.00
ATOM   1154  CE1 TYR A 648      36.659  -4.164  56.884  1.00  0.00
ATOM   1155  CZ  TYR A 648      36.475  -5.484  56.499  1.00  0.00
ATOM   1156  OH  TYR A 648      36.636  -5.838  55.177  1.00  0.00
ATOM   1157  CE2 TYR A 648      36.086  -6.440  57.428  1.00  0.00
ATOM   1158  CD2 TYR A 648      35.868  -6.070  58.749  1.00  0.00
ATOM   1159  C   TYR A 648      34.644  -4.554  62.760  1.00  0.00
ATOM   1160  O   TYR A 648      35.165  -5.231  63.652  1.00  0.00
ATOM   1161  N   VAL A 649      33.814  -3.556  63.019  1.00  0.00
ATOM   1163  CA  VAL A 649      33.677  -3.041  64.383  1.00  0.00
ATOM   1164  CB  VAL A 649      32.892  -1.733  64.329  1.00  0.00
ATOM   1165  CG1 VAL A 649      32.756  -1.115  65.717  1.00  0.00
ATOM   1166  CG2 VAL A 649      33.541  -0.745  63.366  1.00  0.00
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ATOM   1167  C   VAL A 649      32.930  -4.047  65.254  1.00  0.00
ATOM   1168  O   VAL A 649      33.470  -4.481  66.282  1.00  0.00
ATOM   1169  N   SER A 650      31.895  -4.640  64.676  1.00  0.00
ATOM   1171  CA  SER A 650      31.086  -5.614  65.412  1.00  0.00
ATOM   1172  CB  SER A 650      29.793  -5.857  64.640  1.00  0.00
ATOM   1173  OG  SER A 650      29.095  -4.622  64.547  1.00  0.00
ATOM   1174  C   SER A 650      31.823  -6.938  65.594  1.00  0.00
ATOM   1175  O   SER A 650      31.846  -7.458  66.716  1.00  0.00
ATOM   1176  N   SER A 651      32.650  -7.298  64.625  1.00  0.00
ATOM   1178  CA  SER A 651      33.413  -8.544  64.722  1.00  0.00
ATOM   1179  CB  SER A 651      33.898  -8.952  63.334  1.00  0.00
ATOM   1180  OG  SER A 651      34.821  -7.972  62.876  1.00  0.00
ATOM   1181  C   SER A 651      34.616  -8.432  65.654  1.00  0.00
ATOM   1182  O   SER A 651      34.940  -9.426  66.312  1.00  0.00
ATOM   1183  N   GLU A 652      35.105  -7.229  65.915  1.00  0.00
ATOM   1185  CA  GLU A 652      36.214  -7.121  66.865  1.00  0.00
ATOM   1186  CB  GLU A 652      37.029  -5.854  66.628  1.00  0.00
ATOM   1187  CG  GLU A 652      37.621  -5.783  65.223  1.00  0.00
ATOM   1188  CD  GLU A 652      38.337  -7.074  64.835  1.00  0.00
ATOM   1189  OE1 GLU A 652      39.488  -7.223  65.220  1.00  0.00
ATOM   1190  OE2 GLU A 652      37.768  -7.812  64.039  1.00  0.00
ATOM   1191  C   GLU A 652      35.681  -7.130  68.289  1.00  0.00
ATOM   1192  O   GLU A 652      36.244  -7.836  69.133  1.00  0.00
ATOM   1193  N   LEU A 653      34.457  -6.653  68.455  1.00  0.00
ATOM   1195  CA  LEU A 653      33.820  -6.700  69.773  1.00  0.00
ATOM   1196  CB  LEU A 653      32.614  -5.767  69.769  1.00  0.00
ATOM   1197  CG  LEU A 653      33.009  -4.322  69.486  1.00  0.00
ATOM   1198  CD1 LEU A 653      31.778  -3.450  69.281  1.00  0.00
ATOM   1199  CD2 LEU A 653      33.893  -3.754  70.591  1.00  0.00
ATOM   1200  C   LEU A 653      33.358  -8.119  70.093  1.00  0.00
ATOM   1201  O   LEU A 653      33.492  -8.571  71.239  1.00  0.00
ATOM   1202  N   HIS A 654      33.064  -8.866  69.042  1.00  0.00
ATOM   1204  CA  HIS A 654      32.661 -10.264  69.169  1.00  0.00
ATOM   1205  CB  HIS A 654      32.058 -10.685  67.835  1.00  0.00
ATOM   1206  CG  HIS A 654      31.437 -12.066  67.819  1.00  0.00
ATOM   1207  ND1 HIS A 654      32.011 -13.208  67.394  1.00  0.00
ATOM   1209  CE1 HIS A 654      31.136 -14.224  67.531  1.00  0.00
ATOM   1210  NE2 HIS A 654      29.994 -13.716  68.046  1.00  0.00
ATOM   1211  CD2 HIS A 654      30.163 -12.386  68.227  1.00  0.00
ATOM   1212  C   HIS A 654      33.837 -11.173  69.496  1.00  0.00
ATOM   1213  O   HIS A 654      33.816 -11.838  70.538  1.00  0.00
ATOM   1214  N   ARG A 655      34.924 -11.030  68.754  1.00  0.00
ATOM   1216  CA  ARG A 655      36.068 -11.938  68.910  1.00  0.00
ATOM   1217  CB  ARG A 655      36.914 -11.868  67.647  1.00  0.00
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ATOM   1218  CG  ARG A 655      36.146 -12.351  66.425  1.00  0.00
ATOM   1219  CD  ARG A 655      37.008 -12.253  65.172  1.00  0.00
ATOM   1220  NE  ARG A 655      38.220 -13.079  65.312  1.00  0.00
ATOM   1221  CZ  ARG A 655      39.459 -12.590  65.223  1.00  0.00
ATOM   1222  NH1 ARG A 655      39.649 -11.286  65.012  1.00  0.00
ATOM   1223  NH2 ARG A 655      40.509 -13.403  65.365  1.00  0.00
ATOM   1224  C   ARG A 655      36.955 -11.605  70.105  1.00  0.00
ATOM   1225  O   ARG A 655      37.716 -12.464  70.563  1.00  0.00
ATOM   1226  N   LEU A 656      36.832 -10.398  70.628  1.00  0.00
ATOM   1228  CA  LEU A 656      37.541 -10.057  71.861  1.00  0.00
ATOM   1229  CB  LEU A 656      38.003  -8.609  71.766  1.00  0.00
ATOM   1230  CG  LEU A 656      38.995  -8.397  70.626  1.00  0.00
ATOM   1231  CD1 LEU A 656      39.336  -6.918  70.473  1.00  0.00
ATOM   1232  CD2 LEU A 656      40.259  -9.226  70.826  1.00  0.00
ATOM   1233  C   LEU A 656      36.642 -10.241  73.084  1.00  0.00
ATOM   1234  O   LEU A 656      37.136 -10.227  74.220  1.00  0.00
ATOM   1235  N   GLN A 657      35.374 -10.533  72.827  1.00  0.00
ATOM   1237  CA  GLN A 657      34.333 -10.652  73.855  1.00  0.00
ATOM   1238  CB  GLN A 657      34.489 -11.972  74.598  1.00  0.00
ATOM   1239  CG  GLN A 657      34.336 -13.153  73.649  1.00  0.00
ATOM   1240  CD  GLN A 657      34.338 -14.447  74.451  1.00  0.00
ATOM   1241  OE1 GLN A 657      34.424 -15.547  73.892  1.00  0.00
ATOM   1242  NE2 GLN A 657      34.208 -14.295  75.758  1.00  0.00
ATOM   1245  C   GLN A 657      34.383  -9.490  74.831  1.00  0.00
ATOM   1246  O   GLN A 657      34.536  -9.690  76.041  1.00  0.00
ATOM   1247  N   VAL A 658      34.190  -8.295  74.298  1.00  0.00
ATOM   1249  CA  VAL A 658      34.338  -7.073  75.095  1.00  0.00
ATOM   1250  CB  VAL A 658      34.309  -5.890  74.127  1.00  0.00
ATOM   1251  CG1 VAL A 658      34.573  -4.560  74.828  1.00  0.00
ATOM   1252  CG2 VAL A 658      35.324  -6.094  73.011  1.00  0.00
ATOM   1253  C   VAL A 658      33.219  -6.953  76.125  1.00  0.00
ATOM   1254  O   VAL A 658      32.049  -7.210  75.818  1.00  0.00
ATOM   1255  N   SER A 659      33.592  -6.660  77.360  1.00  0.00
ATOM   1257  CA  SER A 659      32.586  -6.398  78.394  1.00  0.00
ATOM   1258  CB  SER A 659      33.231  -6.381  79.775  1.00  0.00
ATOM   1259  OG  SER A 659      33.860  -5.116  79.950  1.00  0.00
ATOM   1260  C   SER A 659      31.954  -5.036  78.149  1.00  0.00
ATOM   1261  O   SER A 659      32.594  -4.138  77.585  1.00  0.00
ATOM   1262  N   TYR A 660      30.798  -4.820  78.754  1.00  0.00
ATOM   1264  CA  TYR A 660      30.094  -3.536  78.604  1.00  0.00
ATOM   1265  CB  TYR A 660      28.631  -3.697  79.031  1.00  0.00
ATOM   1266  CG  TYR A 660      28.387  -4.075  80.495  1.00  0.00
ATOM   1267  CD1 TYR A 660      28.328  -5.412  80.874  1.00  0.00
ATOM   1268  CE1 TYR A 660      28.124  -5.750  82.205  1.00  0.00
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ATOM   1269  CZ  TYR A 660      27.962  -4.749  83.154  1.00  0.00
ATOM   1270  OH  TYR A 660      27.954  -5.075  84.492  1.00  0.00
ATOM   1271  CE2 TYR A 660      27.981  -3.414  82.774  1.00  0.00
ATOM   1272  CD2 TYR A 660      28.186  -3.078  81.443  1.00  0.00
ATOM   1273  C   TYR A 660      30.769  -2.427  79.414  1.00  0.00
ATOM   1274  O   TYR A 660      30.727  -1.258  79.014  1.00  0.00
ATOM   1275  N   GLU A 661      31.580  -2.821  80.382  1.00  0.00
ATOM   1277  CA  GLU A 661      32.356  -1.863  81.164  1.00  0.00
ATOM   1278  CB  GLU A 661      32.890  -2.538  82.428  1.00  0.00
ATOM   1279  CG  GLU A 661      31.786  -2.930  83.412  1.00  0.00
ATOM   1280  CD  GLU A 661      31.495  -4.430  83.375  1.00  0.00
ATOM   1281  OE1 GLU A 661      31.605  -5.001  82.294  1.00  0.00
ATOM   1282  OE2 GLU A 661      31.047  -4.947  84.388  1.00  0.00
ATOM   1283  C   GLU A 661      33.516  -1.338  80.328  1.00  0.00
ATOM   1284  O   GLU A 661      33.669  -0.116  80.202  1.00  0.00
ATOM   1285  N   GLU A 662      34.168  -2.226  79.589  1.00  0.00
ATOM   1287  CA  GLU A 662      35.237  -1.783  78.694  1.00  0.00
ATOM   1288  CB  GLU A 662      35.978  -3.010  78.183  1.00  0.00
ATOM   1289  CG  GLU A 662      36.714  -3.716  79.313  1.00  0.00
ATOM   1290  CD  GLU A 662      37.161  -5.095  78.849  1.00  0.00
ATOM   1291  OE1 GLU A 662      36.307  -5.800  78.324  1.00  0.00
ATOM   1292  OE2 GLU A 662      38.346  -5.380  78.933  1.00  0.00
ATOM   1293  C   GLU A 662      34.684  -0.993  77.516  1.00  0.00
ATOM   1294  O   GLU A 662      35.196   0.101  77.254  1.00  0.00
ATOM   1295  N   TYR A 663      33.509  -1.369  77.035  1.00  0.00
ATOM   1297  CA  TYR A 663      32.888  -0.642  75.925  1.00  0.00
ATOM   1298  CB  TYR A 663      31.658  -1.414  75.460  1.00  0.00
ATOM   1299  CG  TYR A 663      30.799  -0.633  74.468  1.00  0.00
ATOM   1300  CD1 TYR A 663      31.220  -0.482  73.154  1.00  0.00
ATOM   1301  CE1 TYR A 663      30.448   0.246  72.259  1.00  0.00
ATOM   1302  CZ  TYR A 663      29.258   0.822  72.680  1.00  0.00
ATOM   1303  OH  TYR A 663      28.502   1.554  71.793  1.00  0.00
ATOM   1304  CE2 TYR A 663      28.828   0.664  73.990  1.00  0.00
ATOM   1305  CD2 TYR A 663      29.599  -0.067  74.883  1.00  0.00
ATOM   1306  C   TYR A 663      32.464   0.772  76.312  1.00  0.00
ATOM   1307  O   TYR A 663      32.767   1.712  75.568  1.00  0.00
ATOM   1308  N   LEU A 664      32.006   0.957  77.539  1.00  0.00
ATOM   1310  CA  LEU A 664      31.543   2.281  77.966  1.00  0.00
ATOM   1311  CB  LEU A 664      30.705   2.125  79.234  1.00  0.00
ATOM   1312  CG  LEU A 664      29.195   2.219  78.995  1.00  0.00
ATOM   1313  CD1 LEU A 664      28.682   1.260  77.927  1.00  0.00
ATOM   1314  CD2 LEU A 664      28.439   1.986  80.294  1.00  0.00
ATOM   1315  C   LEU A 664      32.712   3.222  78.235  1.00  0.00
ATOM   1316  O   LEU A 664      32.674   4.380  77.794  1.00  0.00
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ATOM   1317  N   CYS A 665      33.828   2.665  78.677  1.00  0.00
ATOM   1319  CA  CYS A 665      35.008   3.493  78.920  1.00  0.00
ATOM   1320  CB  CYS A 665      35.919   2.760  79.890  1.00  0.00
ATOM   1321  SG  CYS A 665      35.186   2.404  81.503  1.00  0.00
ATOM   1322  C   CYS A 665      35.751   3.812  77.623  1.00  0.00
ATOM   1323  O   CYS A 665      36.166   4.962  77.434  1.00  0.00
ATOM   1324  N   MET A 666      35.649   2.927  76.644  1.00  0.00
ATOM   1326  CA  MET A 666      36.238   3.199  75.329  1.00  0.00
ATOM   1327  CB  MET A 666      36.305   1.897  74.543  1.00  0.00
ATOM   1328  CG  MET A 666      37.277   0.904  75.160  1.00  0.00
ATOM   1329  SD  MET A 666      37.151  -0.776  74.512  1.00  0.00
ATOM   1330  CE  MET A 666      37.494  -0.446  72.770  1.00  0.00
ATOM   1331  C   MET A 666      35.396   4.188  74.536  1.00  0.00
ATOM   1332  O   MET A 666      35.958   5.085  73.902  1.00  0.00
ATOM   1333  N   LYS A 667      34.097   4.188  74.779  1.00  0.00
ATOM   1335  CA  LYS A 667      33.199   5.094  74.067  1.00  0.00
ATOM   1336  CB  LYS A 667      31.787   4.547  74.215  1.00  0.00
ATOM   1337  CG  LYS A 667      30.755   5.383  73.466  1.00  0.00
ATOM   1338  CD  LYS A 667      29.323   4.883  73.671  1.00  0.00
ATOM   1339  CE  LYS A 667      28.649   5.412  74.942  1.00  0.00
ATOM   1340  NZ  LYS A 667      29.218   4.876  76.192  1.00  0.00
ATOM   1341  C   LYS A 667      33.283   6.519  74.609  1.00  0.00
ATOM   1342  O   LYS A 667      33.311   7.464  73.811  1.00  0.00
ATOM   1343  N   THR A 668      33.599   6.665  75.888  1.00  0.00
ATOM   1345  CA  THR A 668      33.818   8.020  76.403  1.00  0.00
ATOM   1346  CB  THR A 668      33.497   8.105  77.895  1.00  0.00
ATOM   1347  OG1 THR A 668      33.777   9.433  78.313  1.00  0.00
ATOM   1348  CG2 THR A 668      34.321   7.157  78.755  1.00  0.00
ATOM   1349  C   THR A 668      35.238   8.501  76.095  1.00  0.00
ATOM   1350  O   THR A 668      35.429   9.701  75.866  1.00  0.00
ATOM   1351  N   LEU A 669      36.125   7.567  75.784  1.00  0.00
ATOM   1353  CA  LEU A 669      37.451   7.923  75.277  1.00  0.00
ATOM   1354  CB  LEU A 669      38.407   6.756  75.489  1.00  0.00
ATOM   1355  CG  LEU A 669      38.838   6.653  76.945  1.00  0.00
ATOM   1356  CD1 LEU A 669      39.642   5.381  77.188  1.00  0.00
ATOM   1357  CD2 LEU A 669      39.635   7.888  77.348  1.00  0.00
ATOM   1358  C   LEU A 669      37.419   8.286  73.796  1.00  0.00
ATOM   1359  O   LEU A 669      38.247   9.098  73.378  1.00  0.00
ATOM   1360  N   LEU A 670      36.348   7.935  73.096  1.00  0.00
ATOM   1362  CA  LEU A 670      36.198   8.327  71.687  1.00  0.00
ATOM   1363  CB  LEU A 670      35.195   7.409  71.015  1.00  0.00
ATOM   1364  CG  LEU A 670      35.713   5.986  71.005  1.00  0.00
ATOM   1365  CD1 LEU A 670      34.660   5.048  70.441  1.00  0.00
ATOM   1366  CD2 LEU A 670      37.025   5.893  70.234  1.00  0.00
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ATOM	1367	C	LEU	A	670	35.704	9.756	71.560	1.00	0.00
ATOM	1368	O	LEU	A	670	36.144	10.482	70.659	1.00	0.00
ATOM	1369	N	LEU	A	671	35.085	10.230	72.629	1.00	0.00
ATOM	1371	CA	LEU	A	671	34.688	11.635	72.724	1.00	0.00
ATOM	1372	CB	LEU	A	671	33.669	11.721	73.857	1.00	0.00
ATOM	1373	CG	LEU	A	671	33.128	13.127	74.083	1.00	0.00
ATOM	1374	CD1	LEU	A	671	32.411	13.648	72.844	1.00	0.00
ATOM	1375	CD2	LEU	A	671	32.189	13.138	75.283	1.00	0.00
ATOM	1376	C	LEU	A	671	35.912	12.500	73.040	1.00	0.00
ATOM	1377	O	LEU	A	671	35.968	13.679	72.676	1.00	0.00
ATOM	1378	N	LEU	A	672	36.949	11.845	73.534	1.00	0.00
ATOM	1380	CA	LEU	A	672	38.228	12.482	73.844	1.00	0.00
ATOM	1381	CB	LEU	A	672	38.642	11.993	75.228	1.00	0.00
ATOM	1382	CG	LEU	A	672	37.539	12.238	76.254	1.00	0.00
ATOM	1383	CD1	LEU	A	672	37.761	11.428	77.524	1.00	0.00
ATOM	1384	CD2	LEU	A	672	37.371	13.720	76.568	1.00	0.00
ATOM	1385	C	LEU	A	672	39.321	12.121	72.826	1.00	0.00
ATOM	1386	O	LEU	A	672	40.502	12.367	73.092	1.00	0.00
ATOM	1387	N	SER	A	673	38.950	11.557	71.684	1.00	0.00
ATOM	1389	CA	SER	A	673	39.957	11.067	70.725	1.00	0.00
ATOM	1390	CB	SER	A	673	39.403	9.861	69.974	1.00	0.00
ATOM	1391	OG	SER	A	673	39.316	8.768	70.872	1.00	0.00
ATOM	1392	C	SER	A	673	40.419	12.074	69.675	1.00	0.00
ATOM	1393	O	SER	A	673	41.293	11.728	68.869	1.00	0.00
ATOM	1394	N	SER	A	674	39.854	13.269	69.632	1.00	0.00
ATOM	1396	CA	SER	A	674	40.263	14.210	68.577	1.00	0.00
ATOM	1397	CB	SER	A	674	39.311	14.072	67.394	1.00	0.00
ATOM	1398	OG	SER	A	674	39.394	12.744	66.897	1.00	0.00
ATOM	1399	C	SER	A	674	40.258	15.664	69.030	1.00	0.00
ATOM	1400	O	SER	A	674	39.212	16.210	69.399	1.00	0.00
ATOM	1401	N	VAL	A	675	41.422	16.286	68.964	1.00	0.00
ATOM	1403	CA	VAL	A	675	41.522	17.728	69.218	1.00	0.00
ATOM	1404	CB	VAL	A	675	42.703	17.996	70.152	1.00	0.00
ATOM	1405	CG1	VAL	A	675	42.400	17.553	71.576	1.00	0.00
ATOM	1406	CG2	VAL	A	675	43.990	17.360	69.644	1.00	0.00
ATOM	1407	C	VAL	A	675	41.698	18.466	67.892	1.00	0.00
ATOM	1408	O	VAL	A	675	41.985	17.835	66.870	1.00	0.00
ATOM	1409	N	PRO	A	676	41.413	19.756	67.863	1.00	0.00
ATOM	1410	CA	PRO	A	676	41.889	20.576	66.750	1.00	0.00
ATOM	1411	CB	PRO	A	676	41.325	21.942	66.995	1.00	0.00
ATOM	1412	CG	PRO	A	676	40.664	21.967	68.366	1.00	0.00
ATOM	1413	CD	PRO	A	676	40.797	20.558	68.922	1.00	0.00
ATOM	1414	C	PRO	A	676	43.411	20.598	66.756	1.00	0.00
ATOM	1415	O	PRO	A	676	44.029	20.390	67.807	1.00	0.00

ATOM	1416	N	LYS	A	677	44.010	20.965	65.635	1.00	0.00
ATOM	1418	CA	LYS	A	677	45.478	21.035	65.565	1.00	0.00
ATOM	1419	CB	LYS	A	677	45.874	21.122	64.094	1.00	0.00
ATOM	1420	CG	LYS	A	677	47.359	20.847	63.896	1.00	0.00
ATOM	1421	CD	LYS	A	677	47.714	19.452	64.398	1.00	0.00
ATOM	1422	CE	LYS	A	677	49.199	19.161	64.234	1.00	0.00
ATOM	1423	NZ	LYS	A	677	49.523	17.811	64.721	1.00	0.00
ATOM	1424	C	LYS	A	677	46.051	22.238	66.336	1.00	0.00
ATOM	1425	O	LYS	A	677	47.238	22.253	66.680	1.00	0.00
ATOM	1426	N	ASP	A	678	45.185	23.159	66.730	1.00	0.00
ATOM	1428	CA	ASP	A	678	45.584	24.288	67.577	1.00	0.00
ATOM	1429	CB	ASP	A	678	44.738	25.503	67.209	1.00	0.00
ATOM	1430	CG	ASP	A	678	44.931	25.879	65.742	1.00	0.00
ATOM	1431	OD1	ASP	A	678	44.166	25.385	64.922	1.00	0.00
ATOM	1432	OD2	ASP	A	678	45.846	26.640	65.465	1.00	0.00
ATOM	1433	C	ASP	A	678	45.381	23.999	69.069	1.00	0.00
ATOM	1434	O	ASP	A	678	45.724	24.842	69.905	1.00	0.00
ATOM	1435	N	GLY	A	679	44.829	22.840	69.400	1.00	0.00
ATOM	1437	CA	GLY	A	679	44.537	22.520	70.801	1.00	0.00
ATOM	1438	C	GLY	A	679	43.230	23.158	71.271	1.00	0.00
ATOM	1439	O	GLY	A	679	42.640	24.000	70.582	1.00	0.00
ATOM	1440	N	LEU	A	680	42.752	22.677	72.406	1.00	0.00
ATOM	1442	CA	LEU	A	680	41.547	23.224	73.039	1.00	0.00
ATOM	1443	CB	LEU	A	680	40.853	22.116	73.820	1.00	0.00
ATOM	1444	CG	LEU	A	680	40.336	21.013	72.907	1.00	0.00
ATOM	1445	CD1	LEU	A	680	39.795	19.854	73.729	1.00	0.00
ATOM	1446	CD2	LEU	A	680	39.263	21.541	71.961	1.00	0.00
ATOM	1447	C	LEU	A	680	41.896	24.355	73.999	1.00	0.00
ATOM	1448	O	LEU	A	680	43.008	24.412	74.539	1.00	0.00
ATOM	1449	N	LYS	A	681	40.907	25.182	74.296	1.00	0.00
ATOM	1451	CA	LYS	A	681	41.126	26.285	75.241	1.00	0.00
ATOM	1452	CB	LYS	A	681	39.953	27.253	75.161	1.00	0.00
ATOM	1453	CG	LYS	A	681	40.145	28.427	76.116	1.00	0.00
ATOM	1454	CD	LYS	A	681	39.004	29.427	75.994	1.00	0.00
ATOM	1455	CE	LYS	A	681	39.141	30.567	76.995	1.00	0.00
ATOM	1456	NZ	LYS	A	681	38.007	31.499	76.875	1.00	0.00
ATOM	1457	C	LYS	A	681	41.271	25.748	76.663	1.00	0.00
ATOM	1458	O	LYS	A	681	42.271	26.031	77.333	1.00	0.00
ATOM	1459	N	SER	A	682	40.419	24.800	77.017	1.00	0.00
ATOM	1461	CA	SER	A	682	40.578	24.096	78.295	1.00	0.00
ATOM	1462	CB	SER	A	682	39.226	23.905	78.985	1.00	0.00
ATOM	1463	OG	SER	A	682	38.369	23.114	78.171	1.00	0.00
ATOM	1464	C	SER	A	682	41.279	22.758	78.070	1.00	0.00
ATOM	1465	O	SER	A	682	40.849	21.718	78.590	1.00	0.00

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ATOM   1466  N   GLN A 683      42.462  22.836  77.476  1.00  0.00
ATOM   1468  CA  GLN A 683      43.238  21.646  77.107  1.00  0.00
ATOM   1469  CB  GLN A 683      44.399  22.101  76.227  1.00  0.00
ATOM   1470  CG  GLN A 683      45.280  20.941  75.774  1.00  0.00
ATOM   1471  CD  GLN A 683      44.511  20.017  74.835  1.00  0.00
ATOM   1472  OE1 GLN A 683      43.908  20.471  73.854  1.00  0.00
ATOM   1473  NE2 GLN A 683      44.543  18.734  75.143  1.00  0.00
ATOM   1476  C   GLN A 683      43.800  20.911  78.320  1.00  0.00
ATOM   1477  O   GLN A 683      43.781  19.675  78.332  1.00  0.00
ATOM   1478  N   GLU A 684      43.994  21.625  79.418  1.00  0.00
ATOM   1480  CA  GLU A 684      44.466  20.976  80.645  1.00  0.00
ATOM   1481  CB  GLU A 684      44.894  22.049  81.636  1.00  0.00
ATOM   1482  CG  GLU A 684      45.348  21.434  82.957  1.00  0.00
ATOM   1483  CD  GLU A 684      45.646  22.541  83.962  1.00  0.00
ATOM   1484  OE1 GLU A 684      45.187  23.649  83.718  1.00  0.00
ATOM   1485  OE2 GLU A 684      46.415  22.292  84.879  1.00  0.00
ATOM   1486  C   GLU A 684      43.365  20.129  81.277  1.00  0.00
ATOM   1487  O   GLU A 684      43.616  18.957  81.592  1.00  0.00
ATOM   1488  N   LEU A 685      42.130  20.576  81.116  1.00  0.00
ATOM   1490  CA  LEU A 685      40.990  19.852  81.678  1.00  0.00
ATOM   1491  CB  LEU A 685      39.778  20.773  81.840  1.00  0.00
ATOM   1492  CG  LEU A 685      39.888  21.764  83.001  1.00  0.00
ATOM   1493  CD1 LEU A 685      40.555  23.076  82.590  1.00  0.00
ATOM   1494  CD2 LEU A 685      38.498  22.074  83.546  1.00  0.00
ATOM   1495  C   LEU A 685      40.624  18.688  80.771  1.00  0.00
ATOM   1496  O   LEU A 685      40.301  17.605  81.275  1.00  0.00
ATOM   1497  N   PHE A 686      40.980  18.815  79.503  1.00  0.00
ATOM   1499  CA  PHE A 686      40.797  17.720  78.552  1.00  0.00
ATOM   1500  CB  PHE A 686      40.929  18.281  77.144  1.00  0.00
ATOM   1501  CG  PHE A 686      40.810  17.222  76.056  1.00  0.00
ATOM   1502  CD1 PHE A 686      39.556  16.827  75.612  1.00  0.00
ATOM   1503  CE1 PHE A 686      39.448  15.864  74.617  1.00  0.00
ATOM   1504  CZ  PHE A 686      40.590  15.293  74.075  1.00  0.00
ATOM   1505  CE2 PHE A 686      41.842  15.681  74.528  1.00  0.00
ATOM   1506  CD2 PHE A 686      41.951  16.644  75.518  1.00  0.00
ATOM   1507  C   PHE A 686      41.834  16.622  78.764  1.00  0.00
ATOM   1508  O   PHE A 686      41.484  15.435  78.734  1.00  0.00
ATOM   1509  N   ASP A 687      43.009  17.009  79.235  1.00  0.00
ATOM   1511  CA  ASP A 687      44.052  16.032  79.554  1.00  0.00
ATOM   1512  CB  ASP A 687      45.367  16.760  79.832  1.00  0.00
ATOM   1513  CG  ASP A 687      45.820  17.617  78.652  1.00  0.00
ATOM   1514  OD1 ASP A 687      45.576  17.223  77.517  1.00  0.00
ATOM   1515  OD2 ASP A 687      46.465  18.627  78.900  1.00  0.00
ATOM   1516  C   ASP A 687      43.666  15.261  80.809  1.00  0.00
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ATOM   1517  O   ASP A 687      43.729  14.025  80.821  1.00  0.00
ATOM   1518  N   GLU A 688      43.004  15.955  81.719  1.00  0.00
ATOM   1520  CA  GLU A 688      42.563  15.337  82.968  1.00  0.00
ATOM   1521  CB  GLU A 688      42.176  16.455  83.929  1.00  0.00
ATOM   1522  CG  GLU A 688      43.381  17.329  84.258  1.00  0.00
ATOM   1523  CD  GLU A 688      42.945  18.576  85.021  1.00  0.00
ATOM   1524  OE1 GLU A 688      42.967  19.647  84.424  1.00  0.00
ATOM   1525  OE2 GLU A 688      42.663  18.453  86.203  1.00  0.00
ATOM   1526  C   GLU A 688      41.374  14.400  82.764  1.00  0.00
ATOM   1527  O   GLU A 688      41.423  13.265  83.256  1.00  0.00
ATOM   1528  N   ILE A 689      40.464  14.748  81.867  1.00  0.00
ATOM   1530  CA  ILE A 689      39.301  13.881  81.659  1.00  0.00
ATOM   1531  CB  ILE A 689      38.126  14.675  81.078  1.00  0.00
ATOM   1532  CG2 ILE A 689      38.474  15.414  79.794  1.00  0.00
ATOM   1533  CG1 ILE A 689      36.936  13.762  80.833  1.00  0.00
ATOM   1534  CD1 ILE A 689      35.876  14.443  79.978  1.00  0.00
ATOM   1535  C   ILE A 689      39.631  12.667  80.789  1.00  0.00
ATOM   1536  O   ILE A 689      39.161  11.566  81.112  1.00  0.00
ATOM   1537  N   ARG A 690      40.623  12.770  79.917  1.00  0.00
ATOM   1539  CA  ARG A 690      40.971  11.579  79.148  1.00  0.00
ATOM   1540  CB  ARG A 690      41.551  11.949  77.783  1.00  0.00
ATOM   1541  CG  ARG A 690      42.895  12.665  77.836  1.00  0.00
ATOM   1542  CD  ARG A 690      43.397  12.919  76.422  1.00  0.00
ATOM   1543  NE  ARG A 690      43.374  11.661  75.656  1.00  0.00
ATOM   1544  CZ  ARG A 690      44.370  11.256  74.865  1.00  0.00
ATOM   1545  NH1 ARG A 690      45.445  12.029  74.694  1.00  0.00
ATOM   1546  NH2 ARG A 690      44.276  10.090  74.220  1.00  0.00
ATOM   1547  C   ARG A 690      41.909  10.679  79.944  1.00  0.00
ATOM   1548  O   ARG A 690      41.750   9.456  79.873  1.00  0.00
ATOM   1549  N   MET A 691      42.589  11.250  80.927  1.00  0.00
ATOM   1551  CA  MET A 691      43.444  10.447  81.793  1.00  0.00
ATOM   1552  CB  MET A 691      44.382  11.378  82.550  1.00  0.00
ATOM   1553  CG  MET A 691      45.336  10.604  83.450  1.00  0.00
ATOM   1554  SD  MET A 691      46.473  11.625  84.412  1.00  0.00
ATOM   1555  CE  MET A 691      47.263  12.517  83.052  1.00  0.00
ATOM   1556  C   MET A 691      42.608   9.650  82.784  1.00  0.00
ATOM   1557  O   MET A 691      42.790   8.429  82.870  1.00  0.00
ATOM   1558  N   THR A 692      41.532  10.242  83.281  1.00  0.00
ATOM   1560  CA  THR A 692      40.697   9.504  84.231  1.00  0.00
ATOM   1561  CB  THR A 692      39.910  10.464  85.122  1.00  0.00
ATOM   1562  OG1 THR A 692      39.130   9.675  86.010  1.00  0.00
ATOM   1563  CG2 THR A 692      38.960  11.372  84.350  1.00  0.00
ATOM   1564  C   THR A 692      39.759   8.512  83.544  1.00  0.00
ATOM   1565  O   THR A 692      39.461   7.473  84.142  1.00  0.00
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ATOM	1566	N	TYR A 693	39.505	8.671	82.254	1.00	0.00
ATOM	1568	CA	TYR A 693	38.719	7.647	81.564	1.00	0.00
ATOM	1569	CB	TYR A 693	37.835	8.284	80.503	1.00	0.00
ATOM	1570	CG	TYR A 693	36.652	9.014	81.130	1.00	0.00
ATOM	1571	CD1	TYR A 693	36.047	8.482	82.262	1.00	0.00
ATOM	1572	CE1	TYR A 693	34.978	9.139	82.855	1.00	0.00
ATOM	1573	CZ	TYR A 693	34.511	10.325	82.309	1.00	0.00
ATOM	1574	OH	TYR A 693	33.531	11.038	82.965	1.00	0.00
ATOM	1575	CE2	TYR A 693	35.096	10.847	81.164	1.00	0.00
ATOM	1576	CD2	TYR A 693	36.167	10.189	80.572	1.00	0.00
ATOM	1577	C	TYR A 693	39.602	6.536	81.004	1.00	0.00
ATOM	1578	O	TYR A 693	39.139	5.395	80.894	1.00	0.00
ATOM	1579	N	ILE A 694	40.900	6.789	80.936	1.00	0.00
ATOM	1581	CA	ILE A 694	41.857	5.715	80.653	1.00	0.00
ATOM	1582	CB	ILE A 694	43.156	6.329	80.133	1.00	0.00
ATOM	1583	CG2	ILE A 694	44.301	5.323	80.167	1.00	0.00
ATOM	1584	CG1	ILE A 694	42.973	6.874	78.722	1.00	0.00
ATOM	1585	CD1	ILE A 694	44.247	7.534	78.205	1.00	0.00
ATOM	1586	C	ILE A 694	42.122	4.900	81.918	1.00	0.00
ATOM	1587	O	ILE A 694	42.183	3.666	81.846	1.00	0.00
ATOM	1588	N	LYS A 695	41.981	5.540	83.070	1.00	0.00
ATOM	1590	CA	LYS A 695	42.095	4.818	84.344	1.00	0.00
ATOM	1591	CB	LYS A 695	42.345	5.819	85.467	1.00	0.00
ATOM	1592	CG	LYS A 695	43.629	6.610	85.248	1.00	0.00
ATOM	1593	CD	LYS A 695	44.860	5.711	85.232	1.00	0.00
ATOM	1594	CE	LYS A 695	46.114	6.518	84.918	1.00	0.00
ATOM	1595	NZ	LYS A 695	46.295	7.604	85.894	1.00	0.00
ATOM	1596	C	LYS A 695	40.816	4.045	84.646	1.00	0.00
ATOM	1597	O	LYS A 695	40.882	2.914	85.143	1.00	0.00
ATOM	1598	N	GLU A 696	39.703	4.536	84.126	1.00	0.00
ATOM	1600	CA	GLU A 696	38.431	3.831	84.276	1.00	0.00
ATOM	1601	CB	GLU A 696	37.310	4.828	84.007	1.00	0.00
ATOM	1602	CG	GLU A 696	36.035	4.466	84.758	1.00	0.00
ATOM	1603	CD	GLU A 696	36.250	4.648	86.260	1.00	0.00
ATOM	1604	OE1	GLU A 696	37.071	5.483	86.614	1.00	0.00
ATOM	1605	OE2	GLU A 696	35.496	4.061	87.028	1.00	0.00
ATOM	1606	C	GLU A 696	38.336	2.661	83.296	1.00	0.00
ATOM	1607	O	GLU A 696	37.782	1.615	83.655	1.00	0.00
ATOM	1608	N	LEU A 697	39.057	2.754	82.188	1.00	0.00
ATOM	1610	CA	LEU A 697	39.173	1.624	81.262	1.00	0.00
ATOM	1611	CB	LEU A 697	39.714	2.132	79.929	1.00	0.00
ATOM	1612	CG	LEU A 697	39.845	1.007	78.906	1.00	0.00
ATOM	1613	CD1	LEU A 697	38.505	0.324	78.662	1.00	0.00
ATOM	1614	CD2	LEU A 697	40.432	1.521	77.596	1.00	0.00

ATOM	1615	C	LEU	A	697	40.118	0.578	81.843	1.00	0.00
ATOM	1616	O	LEU	A	697	39.818	-0.618	81.777	1.00	0.00
ATOM	1617	N	GLY	A	698	41.099	1.042	82.599	1.00	0.00
ATOM	1619	CA	GLY	A	698	41.971	0.162	83.383	1.00	0.00
ATOM	1620	C	GLY	A	698	41.155	-0.699	84.343	1.00	0.00
ATOM	1621	O	GLY	A	698	41.166	-1.928	84.213	1.00	0.00
ATOM	1622	N	LYS	A	699	40.282	-0.063	85.112	1.00	0.00
ATOM	1624	CA	LYS	A	699	39.420	-0.783	86.065	1.00	0.00
ATOM	1625	CB	LYS	A	699	38.610	0.252	86.837	1.00	0.00
ATOM	1626	CG	LYS	A	699	39.505	1.316	87.455	1.00	0.00
ATOM	1627	CD	LYS	A	699	38.683	2.417	88.113	1.00	0.00
ATOM	1628	CE	LYS	A	699	39.575	3.563	88.575	1.00	0.00
ATOM	1629	NZ	LYS	A	699	40.615	3.081	89.497	1.00	0.00
ATOM	1630	C	LYS	A	699	38.433	-1.730	85.378	1.00	0.00
ATOM	1631	O	LYS	A	699	38.276	-2.873	85.826	1.00	0.00
ATOM	1632	N	ALA	A	700	37.986	-1.357	84.188	1.00	0.00
ATOM	1634	CA	ALA	A	700	37.053	-2.183	83.417	1.00	0.00
ATOM	1635	CB	ALA	A	700	36.418	-1.286	82.365	1.00	0.00
ATOM	1636	C	ALA	A	700	37.713	-3.382	82.735	1.00	0.00
ATOM	1637	O	ALA	A	700	37.030	-4.363	82.412	1.00	0.00
ATOM	1638	N	ILE	A	701	39.028	-3.347	82.617	1.00	0.00
ATOM	1640	CA	ILE	A	701	39.787	-4.479	82.091	1.00	0.00
ATOM	1641	CB	ILE	A	701	40.988	-3.906	81.354	1.00	0.00
ATOM	1642	CG2	ILE	A	701	41.973	-4.994	80.961	1.00	0.00
ATOM	1643	CG1	ILE	A	701	40.524	-3.137	80.126	1.00	0.00
ATOM	1644	CD1	ILE	A	701	41.686	-2.439	79.438	1.00	0.00
ATOM	1645	C	ILE	A	701	40.232	-5.396	83.224	1.00	0.00
ATOM	1646	O	ILE	A	701	40.054	-6.618	83.111	1.00	0.00
ATOM	1647	N	VAL	A	702	40.413	-4.802	84.395	1.00	0.00
ATOM	1649	CA	VAL	A	702	40.795	-5.550	85.605	1.00	0.00
ATOM	1650	CB	VAL	A	702	41.270	-4.545	86.659	1.00	0.00
ATOM	1651	CG1	VAL	A	702	41.485	-5.186	88.025	1.00	0.00
ATOM	1652	CG2	VAL	A	702	42.541	-3.832	86.217	1.00	0.00
ATOM	1653	C	VAL	A	702	39.641	-6.385	86.170	1.00	0.00
ATOM	1654	O	VAL	A	702	39.893	-7.418	86.804	1.00	0.00
ATOM	1655	N	LYS	A	703	38.422	-6.100	85.736	1.00	0.00
ATOM	1657	CA	LYS	A	703	37.280	-6.927	86.141	1.00	0.00
ATOM	1658	CB	LYS	A	703	35.990	-6.279	85.657	1.00	0.00
ATOM	1659	CG	LYS	A	703	35.699	-4.935	86.305	1.00	0.00
ATOM	1660	CD	LYS	A	703	34.310	-4.472	85.883	1.00	0.00
ATOM	1661	CE	LYS	A	703	33.924	-3.141	86.508	1.00	0.00
ATOM	1662	NZ	LYS	A	703	34.768	-2.050	86.006	1.00	0.00
ATOM	1663	C	LYS	A	703	37.316	-8.335	85.543	1.00	0.00
ATOM	1664	O	LYS	A	703	36.806	-9.271	86.170	1.00	0.00

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ATOM   1665  N   ARG A 704      37.927  -8.503  84.380  1.00  0.00
ATOM   1667  CA  ARG A 704      37.996  -9.844  83.793  1.00  0.00
ATOM   1668  CB  ARG A 704      37.374  -9.815  82.402  1.00  0.00
ATOM   1669  CG  ARG A 704      35.948  -9.277  82.435  1.00  0.00
ATOM   1670  CD  ARG A 704      35.251  -9.473  81.093  1.00  0.00
ATOM   1671  NE  ARG A 704      36.041  -8.896  79.994  1.00  0.00
ATOM   1672  CZ  ARG A 704      36.356  -9.590  78.899  1.00  0.00
ATOM   1673  NH1 ARG A 704      35.981 -10.866  78.786  1.00  0.00
ATOM   1674  NH2 ARG A 704      37.070  -9.018  77.929  1.00  0.00
ATOM   1675  C   ARG A 704      39.432 -10.344  83.692  1.00  0.00
ATOM   1676  O   ARG A 704      39.682 -11.556  83.660  1.00  0.00
ATOM   1677  N   GLU A 705      40.375  -9.420  83.679  1.00  0.00
ATOM   1679  CA  GLU A 705      41.780  -9.806  83.537  1.00  0.00
ATOM   1680  CB  GLU A 705      42.485  -8.792  82.649  1.00  0.00
ATOM   1681  CG  GLU A 705      41.793  -8.633  81.298  1.00  0.00
ATOM   1682  CD  GLU A 705      41.769  -9.943  80.515  1.00  0.00
ATOM   1683  OE1 GLU A 705      42.762 -10.659  80.548  1.00  0.00
ATOM   1684  OE2 GLU A 705      40.754 -10.202  79.886  1.00  0.00
ATOM   1685  C   GLU A 705      42.469  -9.883  84.892  1.00  0.00
ATOM   1686  O   GLU A 705      43.165  -8.952  85.313  1.00  0.00
ATOM   1687  N   GLY A 706      42.318 -11.041  85.516  1.00  0.00
ATOM   1689  CA  GLY A 706      42.921 -11.312  86.826  1.00  0.00
ATOM   1690  C   GLY A 706      44.444 -11.303  86.755  1.00  0.00
ATOM   1691  O   GLY A 706      45.105 -10.616  87.544  1.00  0.00
ATOM   1692  N   ASN A 707      44.985 -12.073  85.825  1.00  0.00
ATOM   1694  CA  ASN A 707      46.434 -12.072  85.604  1.00  0.00
ATOM   1695  CB  ASN A 707      46.780 -13.096  84.526  1.00  0.00
ATOM   1696  CG  ASN A 707      46.228 -14.477  84.870  1.00  0.00
ATOM   1697  OD1 ASN A 707      46.198 -14.886  86.036  1.00  0.00
ATOM   1698  ND2 ASN A 707      45.814 -15.189  83.836  1.00  0.00
ATOM   1701  C   ASN A 707      46.866 -10.691  85.129  1.00  0.00
ATOM   1702  O   ASN A 707      46.345 -10.190  84.126  1.00  0.00
ATOM   1703  N   SER A 708      47.929 -10.173  85.722  1.00  0.00
ATOM   1705  CA  SER A 708      48.365  -8.802  85.408  1.00  0.00
ATOM   1706  CB  SER A 708      49.375  -8.343  86.456  1.00  0.00
ATOM   1707  OG  SER A 708      50.518  -9.187  86.383  1.00  0.00
ATOM   1708  C   SER A 708      48.977  -8.664  84.014  1.00  0.00
ATOM   1709  O   SER A 708      48.712  -7.657  83.348  1.00  0.00
ATOM   1710  N   SER A 709      49.487  -9.759  83.468  1.00  0.00
ATOM   1712  CA  SER A 709      50.000  -9.724  82.096  1.00  0.00
ATOM   1713  CB  SER A 709      50.898 -10.929  81.864  1.00  0.00
ATOM   1714  OG  SER A 709      51.288 -10.898  80.498  1.00  0.00
ATOM   1715  C   SER A 709      48.860  -9.753  81.087  1.00  0.00
ATOM   1716  O   SER A 709      48.912  -9.013  80.099  1.00  0.00
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ATOM   1717  N   GLN A 710      47.734 -10.302  81.514  1.00  0.00
ATOM   1719  CA  GLN A 710      46.533 -10.337  80.686  1.00  0.00
ATOM   1720  CB  GLN A 710      45.613 -11.429  81.217  1.00  0.00
ATOM   1721  CG  GLN A 710      46.048 -12.826  80.804  1.00  0.00
ATOM   1722  CD  GLN A 710      45.774 -13.048  79.319  1.00  0.00
ATOM   1723  OE1 GLN A 710      46.534 -13.753  78.645  1.00  0.00
ATOM   1724  NE2 GLN A 710      44.669 -12.497  78.843  1.00  0.00
ATOM   1727  C   GLN A 710      45.794  -9.011  80.750  1.00  0.00
ATOM   1728  O   GLN A 710      45.195  -8.591  79.753  1.00  0.00
ATOM   1729  N   ASN A 711      46.017  -8.276  81.826  1.00  0.00
ATOM   1731  CA  ASN A 711      45.452  -6.938  81.954  1.00  0.00
ATOM   1732  CB  ASN A 711      45.583  -6.508  83.411  1.00  0.00
ATOM   1733  CG  ASN A 711      45.045  -5.095  83.598  1.00  0.00
ATOM   1734  OD1 ASN A 711      43.838  -4.853  83.497  1.00  0.00
ATOM   1735  ND2 ASN A 711      45.952  -4.167  83.859  1.00  0.00
ATOM   1738  C   ASN A 711      46.196  -5.965  81.050  1.00  0.00
ATOM   1739  O   ASN A 711      45.553  -5.246  80.273  1.00  0.00
ATOM   1740  N   TRP A 712      47.503  -6.147  80.941  1.00  0.00
ATOM   1742  CA  TRP A 712      48.293  -5.279  80.063  1.00  0.00
ATOM   1743  CB  TRP A 712      49.760  -5.349  80.469  1.00  0.00
ATOM   1744  CG  TRP A 712      50.062  -4.651  81.780  1.00  0.00
ATOM   1745  CD1 TRP A 712      50.445  -5.237  82.965  1.00  0.00
ATOM   1746  NE1 TRP A 712      50.616  -4.263  83.892  1.00  0.00
ATOM   1748  CE2 TRP A 712      50.371  -3.047  83.372  1.00  0.00
ATOM   1749  CZ2 TRP A 712      50.416  -1.767  83.905  1.00  0.00
ATOM   1750  CH2 TRP A 712      50.108  -0.674  83.103  1.00  0.00
ATOM   1751  CZ3 TRP A 712      49.757  -0.857  81.769  1.00  0.00
ATOM   1752  CE3 TRP A 712      49.710  -2.135  81.226  1.00  0.00
ATOM   1753  CD2 TRP A 712      50.016  -3.228  82.022  1.00  0.00
ATOM   1754  C   TRP A 712      48.150  -5.650  78.591  1.00  0.00
ATOM   1755  O   TRP A 712      48.091  -4.747  77.745  1.00  0.00
ATOM   1756  N   GLN A 713      47.865  -6.913  78.312  1.00  0.00
ATOM   1758  CA  GLN A 713      47.625  -7.321  76.926  1.00  0.00
ATOM   1759  CB  GLN A 713      47.658  -8.842  76.819  1.00  0.00
ATOM   1760  CG  GLN A 713      49.051  -9.411  77.069  1.00  0.00
ATOM   1761  CD  GLN A 713      50.036  -8.933  76.005  1.00  0.00
ATOM   1762  OE1 GLN A 713      49.954  -9.335  74.839  1.00  0.00
ATOM   1763  NE2 GLN A 713      50.996  -8.130  76.433  1.00  0.00
ATOM   1766  C   GLN A 713      46.275  -6.813  76.456  1.00  0.00
ATOM   1767  O   GLN A 713      46.233  -6.074  75.466  1.00  0.00
ATOM   1768  N   ARG A 714      45.304  -6.867  77.352  1.00  0.00
ATOM   1770  CA  ARG A 714      43.946  -6.435  77.035  1.00  0.00
ATOM   1771  CB  ARG A 714      43.065  -6.919  78.173  1.00  0.00
ATOM   1772  CG  ARG A 714      41.592  -6.780  77.843  1.00  0.00
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ATOM   1773  CD  ARG A 714      41.216  -7.730  76.722  1.00  0.00
ATOM   1774  NE  ARG A 714      39.804  -7.551  76.386  1.00  0.00
ATOM   1775  CZ  ARG A 714      39.396  -7.227  75.162  1.00  0.00
ATOM   1776  NH1 ARG A 714      40.287  -7.095  74.177  1.00  0.00
ATOM   1777  NH2 ARG A 714      38.096  -7.050  74.925  1.00  0.00
ATOM   1778  C   ARG A 714      43.837  -4.916  76.921  1.00  0.00
ATOM   1779  O   ARG A 714      43.162  -4.416  76.011  1.00  0.00
ATOM   1780  N   PHE A 715      44.666  -4.204  77.668  1.00  0.00
ATOM   1782  CA  PHE A 715      44.694  -2.744  77.557  1.00  0.00
ATOM   1783  CB  PHE A 715      45.456  -2.173  78.747  1.00  0.00
ATOM   1784  CG  PHE A 715      45.507  -0.648  78.774  1.00  0.00
ATOM   1785  CD1 PHE A 715      44.386   0.074  79.162  1.00  0.00
ATOM   1786  CE1 PHE A 715      44.426   1.462  79.184  1.00  0.00
ATOM   1787  CZ  PHE A 715      45.589   2.127  78.817  1.00  0.00
ATOM   1788  CE2 PHE A 715      46.710   1.406  78.429  1.00  0.00
ATOM   1789  CD2 PHE A 715      46.669   0.018  78.407  1.00  0.00
ATOM   1790  C   PHE A 715      45.358  -2.305  76.257  1.00  0.00
ATOM   1791  O   PHE A 715      44.796  -1.461  75.544  1.00  0.00
ATOM   1792  N   TYR A 716      46.358  -3.055  75.824  1.00  0.00
ATOM   1794  CA  TYR A 716      47.011  -2.746  74.553  1.00  0.00
ATOM   1795  CB  TYR A 716      48.307  -3.542  74.446  1.00  0.00
ATOM   1796  CG  TYR A 716      49.046  -3.324  73.128  1.00  0.00
ATOM   1797  CD1 TYR A 716      49.801  -2.173  72.944  1.00  0.00
ATOM   1798  CE1 TYR A 716      50.465  -1.963  71.743  1.00  0.00
ATOM   1799  CZ  TYR A 716      50.370  -2.905  70.728  1.00  0.00
ATOM   1800  OH  TYR A 716      50.984  -2.671  69.518  1.00  0.00
ATOM   1801  CE2 TYR A 716      49.621  -4.060  70.910  1.00  0.00
ATOM   1802  CD2 TYR A 716      48.959  -4.270  72.112  1.00  0.00
ATOM   1803  C   TYR A 716      46.101  -3.094  73.381  1.00  0.00
ATOM   1804  O   TYR A 716      45.947  -2.262  72.480  1.00  0.00
ATOM   1805  N   GLN A 717      45.312  -4.145  73.533  1.00  0.00
ATOM   1807  CA  GLN A 717      44.381  -4.561  72.482  1.00  0.00
ATOM   1808  CB  GLN A 717      43.806  -5.917  72.864  1.00  0.00
ATOM   1809  CG  GLN A 717      44.881  -6.993  72.925  1.00  0.00
ATOM   1810  CD  GLN A 717      44.287  -8.261  73.526  1.00  0.00
ATOM   1811  OE1 GLN A 717      44.686  -8.711  74.609  1.00  0.00
ATOM   1812  NE2 GLN A 717      43.299  -8.796  72.832  1.00  0.00
ATOM   1815  C   GLN A 717      43.227  -3.581  72.311  1.00  0.00
ATOM   1816  O   GLN A 717      42.932  -3.196  71.174  1.00  0.00
ATOM   1817  N   LEU A 718      42.745  -3.011  73.402  1.00  0.00
ATOM   1819  CA  LEU A 718      41.625  -2.072  73.293  1.00  0.00
ATOM   1820  CB  LEU A 718      40.925  -1.980  74.640  1.00  0.00
ATOM   1821  CG  LEU A 718      40.260  -3.307  74.984  1.00  0.00
ATOM   1822  CD1 LEU A 718      39.617  -3.258  76.364  1.00  0.00
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ATOM	1823	CD2	LEU	A	718	39.239	-3.689	73.919	1.00	0.00
ATOM	1824	C	LEU	A	718	42.065	-0.690	72.834	1.00	0.00
ATOM	1825	O	LEU	A	718	41.383	-0.090	71.994	1.00	0.00
ATOM	1826	N	THR	A	719	43.294	-0.319	73.150	1.00	0.00
ATOM	1828	CA	THR	A	719	43.803	0.973	72.678	1.00	0.00
ATOM	1829	CB	THR	A	719	44.932	1.455	73.583	1.00	0.00
ATOM	1830	OG1	THR	A	719	45.962	0.476	73.610	1.00	0.00
ATOM	1831	CG2	THR	A	719	44.443	1.695	75.006	1.00	0.00
ATOM	1832	C	THR	A	719	44.285	0.896	71.231	1.00	0.00
ATOM	1833	O	THR	A	719	44.076	1.847	70.466	1.00	0.00
ATOM	1834	N	LYS	A	720	44.662	-0.295	70.796	1.00	0.00
ATOM	1836	CA	LYS	A	720	45.050	-0.483	69.400	1.00	0.00
ATOM	1837	CB	LYS	A	720	45.947	-1.711	69.304	1.00	0.00
ATOM	1838	CG	LYS	A	720	46.557	-1.838	67.917	1.00	0.00
ATOM	1839	CD	LYS	A	720	47.389	-0.605	67.580	1.00	0.00
ATOM	1840	CE	LYS	A	720	47.988	-0.717	66.186	1.00	0.00
ATOM	1841	NZ	LYS	A	720	48.859	-1.900	66.083	1.00	0.00
ATOM	1842	C	LYS	A	720	43.814	-0.663	68.524	1.00	0.00
ATOM	1843	O	LYS	A	720	43.795	-0.186	67.381	1.00	0.00
ATOM	1844	N	LEU	A	721	42.727	-1.092	69.143	1.00	0.00
ATOM	1846	CA	LEU	A	721	41.447	-1.157	68.445	1.00	0.00
ATOM	1847	CB	LEU	A	721	40.451	-1.930	69.304	1.00	0.00
ATOM	1848	CG	LEU	A	721	39.100	-2.072	68.610	1.00	0.00
ATOM	1849	CD1	LEU	A	721	39.251	-2.767	67.260	1.00	0.00
ATOM	1850	CD2	LEU	A	721	38.111	-2.824	69.493	1.00	0.00
ATOM	1851	C	LEU	A	721	40.925	0.250	68.195	1.00	0.00
ATOM	1852	O	LEU	A	721	40.699	0.591	67.029	1.00	0.00
ATOM	1853	N	LEU	A	722	41.072	1.123	69.181	1.00	0.00
ATOM	1855	CA	LEU	A	722	40.635	2.514	69.010	1.00	0.00
ATOM	1856	CB	LEU	A	722	40.666	3.213	70.366	1.00	0.00
ATOM	1857	CG	LEU	A	722	39.721	2.552	71.362	1.00	0.00
ATOM	1858	CD1	LEU	A	722	39.850	3.185	72.743	1.00	0.00
ATOM	1859	CD2	LEU	A	722	38.276	2.602	70.876	1.00	0.00
ATOM	1860	C	LEU	A	722	41.535	3.267	68.033	1.00	0.00
ATOM	1861	O	LEU	A	722	41.022	3.962	67.146	1.00	0.00
ATOM	1862	N	ASP	A	723	42.808	2.903	68.008	1.00	0.00
ATOM	1864	CA	ASP	A	723	43.753	3.502	67.059	1.00	0.00
ATOM	1865	CB	ASP	A	723	45.157	3.007	67.384	1.00	0.00
ATOM	1866	CG	ASP	A	723	45.766	3.774	68.552	1.00	0.00
ATOM	1867	OD1	ASP	A	723	45.032	4.465	69.245	1.00	0.00
ATOM	1868	OD2	ASP	A	723	46.979	3.922	68.525	1.00	0.00
ATOM	1869	C	ASP	A	723	43.437	3.124	65.616	1.00	0.00
ATOM	1870	O	ASP	A	723	43.224	4.020	64.786	1.00	0.00
ATOM	1871	N	SER	A	724	43.128	1.855	65.402	1.00	0.00

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ATOM   1873  CA  SER A 724      42.847   1.355  64.051  1.00  0.00
ATOM   1874  CB  SER A 724      43.057  -0.155  64.032  1.00  0.00
ATOM   1875  OG  SER A 724      42.110  -0.747  64.913  1.00  0.00
ATOM   1876  C   SER A 724      41.427   1.668  63.583  1.00  0.00
ATOM   1877  O   SER A 724      41.164   1.639  62.375  1.00  0.00
ATOM   1878  N   MET A 725      40.578   2.143  64.478  1.00  0.00
ATOM   1880  CA  MET A 725      39.226   2.522  64.079  1.00  0.00
ATOM   1881  CB  MET A 725      38.302   2.427  65.279  1.00  0.00
ATOM   1882  CG  MET A 725      38.024   0.986  65.707  1.00  0.00
ATOM   1883  SD  MET A 725      37.134  -0.071  64.538  1.00  0.00
ATOM   1884  CE  MET A 725      38.513  -0.893  63.704  1.00  0.00
ATOM   1885  C   MET A 725      39.156   3.918  63.468  1.00  0.00
ATOM   1886  O   MET A 725      38.213   4.182  62.711  1.00  0.00
ATOM   1887  N   HIS A 726      40.243   4.672  63.521  1.00  0.00
ATOM   1889  CA  HIS A 726      40.255   5.971  62.835  1.00  0.00
ATOM   1890  CB  HIS A 726      41.453   6.792  63.301  1.00  0.00
ATOM   1891  CG  HIS A 726      41.413   7.237  64.751  1.00  0.00
ATOM   1892  ND1 HIS A 726      42.077   6.678  65.778  1.00  0.00
ATOM   1894  CE1 HIS A 726      41.801   7.352  66.912  1.00  0.00
ATOM   1895  NE2 HIS A 726      40.951   8.354  66.594  1.00  0.00
ATOM   1896  CD2 HIS A 726      40.703   8.296  65.265  1.00  0.00
ATOM   1897  C   HIS A 726      40.328   5.806  61.313  1.00  0.00
ATOM   1898  O   HIS A 726      39.691   6.590  60.596  1.00  0.00
ATOM   1899  N   GLU A 727      40.784   4.645  60.861  1.00  0.00
ATOM   1901  CA  GLU A 727      40.862   4.406  59.420  1.00  0.00
ATOM   1902  CB  GLU A 727      41.940   3.360  59.128  1.00  0.00
ATOM   1903  CG  GLU A 727      41.508   1.935  59.457  1.00  0.00
ATOM   1904  CD  GLU A 727      42.735   1.062  59.699  1.00  0.00
ATOM   1905  OE1 GLU A 727      43.667   1.562  60.314  1.00  0.00
ATOM   1906  OE2 GLU A 727      42.694  -0.104  59.329  1.00  0.00
ATOM   1907  C   GLU A 727      39.510   3.996  58.827  1.00  0.00
ATOM   1908  O   GLU A 727      39.299   4.245  57.637  1.00  0.00
ATOM   1909  N   VAL A 728      38.551   3.604  59.657  1.00  0.00
ATOM   1911  CA  VAL A 728      37.213   3.338  59.131  1.00  0.00
ATOM   1912  CB  VAL A 728      36.630   2.052  59.725  1.00  0.00
ATOM   1913  CG1 VAL A 728      36.806   1.943  61.232  1.00  0.00
ATOM   1914  CG2 VAL A 728      35.167   1.866  59.344  1.00  0.00
ATOM   1915  C   VAL A 728      36.312   4.549  59.359  1.00  0.00
ATOM   1916  O   VAL A 728      35.470   4.864  58.506  1.00  0.00
ATOM   1917  N   VAL A 729      36.704   5.392  60.302  1.00  0.00
ATOM   1919  CA  VAL A 729      35.952   6.625  60.544  1.00  0.00
ATOM   1920  CB  VAL A 729      36.318   7.170  61.921  1.00  0.00
ATOM   1921  CG1 VAL A 729      35.681   8.532  62.178  1.00  0.00
ATOM   1922  CG2 VAL A 729      35.909   6.187  63.006  1.00  0.00
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ATOM	1923	C	VAL	A	729	36.240	7.665	59.467	1.00	0.00
ATOM	1924	O	VAL	A	729	35.314	8.371	59.048	1.00	0.00
ATOM	1925	N	GLU	A	730	37.387	7.547	58.817	1.00	0.00
ATOM	1927	CA	GLU	A	730	37.669	8.451	57.702	1.00	0.00
ATOM	1928	CB	GLU	A	730	39.179	8.568	57.497	1.00	0.00
ATOM	1929	CG	GLU	A	730	39.825	7.247	57.100	1.00	0.00
ATOM	1930	CD	GLU	A	730	41.345	7.378	57.066	1.00	0.00
ATOM	1931	OE1	GLU	A	730	41.868	7.723	56.017	1.00	0.00
ATOM	1932	OE2	GLU	A	730	41.955	7.126	58.097	1.00	0.00
ATOM	1933	C	GLU	A	730	36.962	8.028	56.408	1.00	0.00
ATOM	1934	O	GLU	A	730	36.682	8.908	55.584	1.00	0.00
ATOM	1935	N	ASN	A	731	36.484	6.794	56.300	1.00	0.00
ATOM	1937	CA	ASN	A	731	35.678	6.471	55.120	1.00	0.00
ATOM	1938	CB	ASN	A	731	35.961	5.068	54.567	1.00	0.00
ATOM	1939	CG	ASN	A	731	35.700	3.917	55.540	1.00	0.00
ATOM	1940	OD1	ASN	A	731	36.640	3.383	56.136	1.00	0.00
ATOM	1941	ND2	ASN	A	731	34.461	3.453	55.575	1.00	0.00
ATOM	1944	C	ASN	A	731	34.201	6.685	55.429	1.00	0.00
ATOM	1945	O	ASN	A	731	33.451	7.073	54.525	1.00	0.00
ATOM	1946	N	LEU	A	732	33.871	6.721	56.712	1.00	0.00
ATOM	1948	CA	LEU	A	732	32.508	7.055	57.132	1.00	0.00
ATOM	1949	CB	LEU	A	732	32.348	6.743	58.617	1.00	0.00
ATOM	1950	CG	LEU	A	732	32.443	5.254	58.924	1.00	0.00
ATOM	1951	CD1	LEU	A	732	32.476	5.011	60.429	1.00	0.00
ATOM	1952	CD2	LEU	A	732	31.300	4.481	58.283	1.00	0.00
ATOM	1953	C	LEU	A	732	32.250	8.539	56.917	1.00	0.00
ATOM	1954	O	LEU	A	732	31.232	8.906	56.320	1.00	0.00
ATOM	1955	N	LEU	A	733	33.270	9.346	57.162	1.00	0.00
ATOM	1957	CA	LEU	A	733	33.158	10.786	56.917	1.00	0.00
ATOM	1958	CB	LEU	A	733	34.283	11.487	57.664	1.00	0.00
ATOM	1959	CG	LEU	A	733	34.013	11.480	59.164	1.00	0.00
ATOM	1960	CD1	LEU	A	733	35.251	11.870	59.959	1.00	0.00
ATOM	1961	CD2	LEU	A	733	32.837	12.389	59.502	1.00	0.00
ATOM	1962	C	LEU	A	733	33.222	11.133	55.433	1.00	0.00
ATOM	1963	O	LEU	A	733	32.441	11.983	54.989	1.00	0.00
ATOM	1964	N	ASN	A	734	33.921	10.327	54.649	1.00	0.00
ATOM	1966	CA	ASN	A	734	33.948	10.554	53.202	1.00	0.00
ATOM	1967	CB	ASN	A	734	35.056	9.724	52.564	1.00	0.00
ATOM	1968	CG	ASN	A	734	36.277	10.603	52.322	1.00	0.00
ATOM	1969	OD1	ASN	A	734	36.316	11.379	51.356	1.00	0.00
ATOM	1970	ND2	ASN	A	734	37.239	10.513	53.222	1.00	0.00
ATOM	1973	C	ASN	A	734	32.621	10.201	52.550	1.00	0.00
ATOM	1974	O	ASN	A	734	32.024	11.078	51.910	1.00	0.00
ATOM	1975	N	TYR	A	735	32.033	9.089	52.962	1.00	0.00

ATOM	1977	CA	TYR A 735	30.776	8.654	52.354	1.00	0.00
ATOM	1978	CB	TYR A 735	30.563	7.180	52.673	1.00	0.00
ATOM	1979	CG	TYR A 735	29.561	6.466	51.767	1.00	0.00
ATOM	1980	CD1	TYR A 735	30.027	5.739	50.680	1.00	0.00
ATOM	1981	CE1	TYR A 735	29.133	5.077	49.850	1.00	0.00
ATOM	1982	CZ	TYR A 735	27.772	5.144	50.110	1.00	0.00
ATOM	1983	OH	TYR A 735	26.888	4.463	49.302	1.00	0.00
ATOM	1984	CE2	TYR A 735	27.300	5.869	51.196	1.00	0.00
ATOM	1985	CD2	TYR A 735	28.197	6.530	52.027	1.00	0.00
ATOM	1986	C	TYR A 735	29.597	9.475	52.867	1.00	0.00
ATOM	1987	O	TYR A 735	28.729	9.847	52.067	1.00	0.00
ATOM	1988	N	CYS A 736	29.696	9.977	54.086	1.00	0.00
ATOM	1990	CA	CYS A 736	28.640	10.843	54.608	1.00	0.00
ATOM	1991	CB	CYS A 736	28.826	11.008	56.111	1.00	0.00
ATOM	1992	SG	CYS A 736	27.633	12.095	56.926	1.00	0.00
ATOM	1993	C	CYS A 736	28.678	12.217	53.952	1.00	0.00
ATOM	1994	O	CYS A 736	27.638	12.677	53.463	1.00	0.00
ATOM	1995	N	PHE A 737	29.874	12.713	53.681	1.00	0.00
ATOM	1997	CA	PHE A 737	30.000	14.042	53.085	1.00	0.00
ATOM	1998	CB	PHE A 737	31.431	14.524	53.302	1.00	0.00
ATOM	1999	CG	PHE A 737	31.671	15.997	52.981	1.00	0.00
ATOM	2000	CD1	PHE A 737	32.188	16.373	51.749	1.00	0.00
ATOM	2001	CE1	PHE A 737	32.408	17.715	51.468	1.00	0.00
ATOM	2002	CZ	PHE A 737	32.115	18.681	52.422	1.00	0.00
ATOM	2003	CE2	PHE A 737	31.605	18.305	53.658	1.00	0.00
ATOM	2004	CD2	PHE A 737	31.385	16.963	53.938	1.00	0.00
ATOM	2005	C	PHE A 737	29.667	14.017	51.595	1.00	0.00
ATOM	2006	O	PHE A 737	28.942	14.905	51.128	1.00	0.00
ATOM	2007	N	GLN A 738	29.943	12.909	50.926	1.00	0.00
ATOM	2009	CA	GLN A 738	29.590	12.836	49.508	1.00	0.00
ATOM	2010	CB	GLN A 738	30.484	11.829	48.788	1.00	0.00
ATOM	2011	CG	GLN A 738	30.307	10.413	49.320	1.00	0.00
ATOM	2012	CD	GLN A 738	31.187	9.439	48.556	1.00	0.00
ATOM	2013	OE1	GLN A 738	32.012	8.728	49.143	1.00	0.00
ATOM	2014	NE2	GLN A 738	30.969	9.395	47.253	1.00	0.00
ATOM	2017	C	GLN A 738	28.117	12.485	49.304	1.00	0.00
ATOM	2018	O	GLN A 738	27.521	13.009	48.357	1.00	0.00
ATOM	2019	N	THR A 739	27.470	11.882	50.290	1.00	0.00
ATOM	2021	CA	THR A 739	26.043	11.590	50.149	1.00	0.00
ATOM	2022	CB	THR A 739	25.707	10.354	50.976	1.00	0.00
ATOM	2023	OG1	THR A 739	26.490	9.280	50.474	1.00	0.00
ATOM	2024	CG2	THR A 739	24.244	9.956	50.836	1.00	0.00
ATOM	2025	C	THR A 739	25.210	12.791	50.584	1.00	0.00
ATOM	2026	O	THR A 739	24.126	13.016	50.036	1.00	0.00

ATOM	2027	N	PHE	A	740	25.831	13.668	51.357	1.00	0.00
ATOM	2029	CA	PHE	A	740	25.223	14.951	51.711	1.00	0.00
ATOM	2030	CB	PHE	A	740	25.918	15.449	52.977	1.00	0.00
ATOM	2031	CG	PHE	A	740	25.552	16.861	53.426	1.00	0.00
ATOM	2032	CD1	PHE	A	740	24.342	17.098	54.065	1.00	0.00
ATOM	2033	CE1	PHE	A	740	24.014	18.385	54.476	1.00	0.00
ATOM	2034	CZ	PHE	A	740	24.897	19.433	54.249	1.00	0.00
ATOM	2035	CE2	PHE	A	740	26.108	19.195	53.613	1.00	0.00
ATOM	2036	CD2	PHE	A	740	26.435	17.910	53.202	1.00	0.00
ATOM	2037	C	PHE	A	740	25.395	15.974	50.589	1.00	0.00
ATOM	2038	O	PHE	A	740	24.533	16.840	50.406	1.00	0.00
ATOM	2039	N	LEU	A	741	26.410	15.794	49.761	1.00	0.00
ATOM	2041	CA	LEU	A	741	26.590	16.683	48.610	1.00	0.00
ATOM	2042	CB	LEU	A	741	28.076	16.651	48.237	1.00	0.00
ATOM	2043	CG	LEU	A	741	28.511	17.759	47.275	1.00	0.00
ATOM	2044	CD1	LEU	A	741	28.244	17.441	45.806	1.00	0.00
ATOM	2045	CD2	LEU	A	741	27.939	19.115	47.679	1.00	0.00
ATOM	2046	C	LEU	A	741	25.716	16.199	47.454	1.00	0.00
ATOM	2047	O	LEU	A	741	24.995	16.990	46.834	1.00	0.00
ATOM	2048	N	ASP	A	742	25.600	14.886	47.350	1.00	0.00
ATOM	2050	CA	ASP	A	742	24.803	14.248	46.298	1.00	0.00
ATOM	2051	CB	ASP	A	742	25.404	12.878	45.973	1.00	0.00
ATOM	2052	CG	ASP	A	742	26.853	12.975	45.486	1.00	0.00
ATOM	2053	OD1	ASP	A	742	27.193	13.990	44.894	1.00	0.00
ATOM	2054	OD2	ASP	A	742	27.564	11.985	45.621	1.00	0.00
ATOM	2055	C	ASP	A	742	23.342	14.041	46.697	1.00	0.00
ATOM	2056	O	ASP	A	742	22.604	13.408	45.930	1.00	0.00
ATOM	2057	N	LYS	A	743	22.876	14.718	47.737	1.00	0.00
ATOM	2059	CA	LYS	A	743	21.573	14.391	48.333	1.00	0.00
ATOM	2060	CB	LYS	A	743	21.478	15.004	49.738	1.00	0.00
ATOM	2061	CG	LYS	A	743	20.899	16.419	49.850	1.00	0.00
ATOM	2062	CD	LYS	A	743	21.811	17.518	49.317	1.00	0.00
ATOM	2063	CE	LYS	A	743	21.271	18.900	49.659	1.00	0.00
ATOM	2064	NZ	LYS	A	743	21.189	19.068	51.120	1.00	0.00
ATOM	2065	C	LYS	A	743	20.366	14.786	47.477	1.00	0.00
ATOM	2066	O	LYS	A	743	19.344	14.092	47.546	1.00	0.00
ATOM	2067	N	THR	A	744	20.570	15.639	46.484	1.00	0.00
ATOM	2069	CA	THR	A	744	19.469	15.997	45.582	1.00	0.00
ATOM	2070	CB	THR	A	744	19.745	17.370	44.978	1.00	0.00
ATOM	2071	OG1	THR	A	744	20.919	17.288	44.180	1.00	0.00
ATOM	2072	CG2	THR	A	744	19.958	18.433	46.048	1.00	0.00
ATOM	2073	C	THR	A	744	19.299	14.988	44.445	1.00	0.00
ATOM	2074	O	THR	A	744	18.212	14.896	43.869	1.00	0.00
ATOM	2075	N	MET	A	745	20.311	14.168	44.209	1.00	0.00

ATOM	2077	CA	MET	A	745	20.236	13.170	43.139	1.00	0.00
ATOM	2078	CB	MET	A	745	21.533	13.239	42.344	1.00	0.00
ATOM	2079	CG	MET	A	745	21.761	14.636	41.776	1.00	0.00
ATOM	2080	SD	MET	A	745	23.344	14.883	40.942	1.00	0.00
ATOM	2081	CE	MET	A	745	24.446	14.543	42.335	1.00	0.00
ATOM	2082	C	MET	A	745	20.077	11.775	43.729	1.00	0.00
ATOM	2083	O	MET	A	745	19.551	10.856	43.091	1.00	0.00
ATOM	2084	N	SER	A	746	20.503	11.654	44.975	1.00	0.00
ATOM	2086	CA	SER	A	746	20.402	10.392	45.711	1.00	0.00
ATOM	2087	CB	SER	A	746	21.629	10.242	46.602	1.00	0.00
ATOM	2088	OG	SER	A	746	21.556	11.239	47.615	1.00	0.00
ATOM	2089	C	SER	A	746	19.158	10.337	46.590	1.00	0.00
ATOM	2090	O	SER	A	746	19.008	9.374	47.348	1.00	0.00
ATOM	2091	N	ILE	A	747	18.336	11.377	46.524	1.00	0.00
ATOM	2093	CA	ILE	A	747	17.112	11.507	47.332	1.00	0.00
ATOM	2094	CB	ILE	A	747	16.026	10.602	46.752	1.00	0.00
ATOM	2095	CG2	ILE	A	747	14.708	10.772	47.504	1.00	0.00
ATOM	2096	CG1	ILE	A	747	15.805	10.913	45.273	1.00	0.00
ATOM	2097	CD1	ILE	A	747	15.255	12.322	45.067	1.00	0.00
ATOM	2098	C	ILE	A	747	17.419	11.188	48.795	1.00	0.00
ATOM	2099	O	ILE	A	747	17.033	10.149	49.343	1.00	0.00
ATOM	2100	N	GLU	A	748	18.256	12.039	49.358	1.00	0.00
ATOM	2102	CA	GLU	A	748	18.735	11.844	50.721	1.00	0.00
ATOM	2103	CB	GLU	A	748	20.233	11.562	50.637	1.00	0.00
ATOM	2104	CG	GLU	A	748	20.802	10.962	51.916	1.00	0.00
ATOM	2105	CD	GLU	A	748	21.747	11.941	52.609	1.00	0.00
ATOM	2106	OE1	GLU	A	748	21.634	13.127	52.348	1.00	0.00
ATOM	2107	OE2	GLU	A	748	22.562	11.485	53.405	1.00	0.00
ATOM	2108	C	GLU	A	748	18.430	13.109	51.510	1.00	0.00
ATOM	2109	O	GLU	A	748	18.682	14.219	51.032	1.00	0.00
ATOM	2110	N	PHE	A	749	17.851	12.949	52.686	1.00	0.00
ATOM	2112	CA	PHE	A	749	17.424	14.129	53.448	1.00	0.00
ATOM	2113	CB	PHE	A	749	15.901	14.222	53.402	1.00	0.00
ATOM	2114	CG	PHE	A	749	15.320	14.358	51.997	1.00	0.00
ATOM	2115	CD1	PHE	A	749	14.561	13.327	51.454	1.00	0.00
ATOM	2116	CE1	PHE	A	749	14.039	13.450	50.173	1.00	0.00
ATOM	2117	CZ	PHE	A	749	14.272	14.603	49.436	1.00	0.00
ATOM	2118	CE2	PHE	A	749	15.024	15.635	49.982	1.00	0.00
ATOM	2119	CD2	PHE	A	749	15.546	15.514	51.262	1.00	0.00
ATOM	2120	C	PHE	A	749	17.880	14.066	54.900	1.00	0.00
ATOM	2121	O	PHE	A	749	17.137	13.594	55.768	1.00	0.00
ATOM	2122	N	PRO	A	750	19.079	14.561	55.161	1.00	0.00
ATOM	2123	CA	PRO	A	750	19.544	14.689	56.537	1.00	0.00
ATOM	2124	CB	PRO	A	750	21.007	14.988	56.426	1.00	0.00

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ATOM   2125  CG  PRO A 750      21.327  15.328  54.979  1.00  0.00
ATOM   2126  CD  PRO A 750      20.030  15.135  54.206  1.00  0.00
ATOM   2127  C   PRO A 750      18.805  15.823  57.230  1.00  0.00
ATOM   2128  O   PRO A 750      18.674  16.918  56.677  1.00  0.00
ATOM   2129  N   GLU A 751      18.336  15.561  58.436  1.00  0.00
ATOM   2131  CA  GLU A 751      17.700  16.620  59.228  1.00  0.00
ATOM   2132  CB  GLU A 751      17.037  16.006  60.451  1.00  0.00
ATOM   2133  CG  GLU A 751      18.001  15.153  61.262  1.00  0.00
ATOM   2134  CD  GLU A 751      17.227  14.486  62.389  1.00  0.00
ATOM   2135  OE1 GLU A 751      16.771  13.371  62.177  1.00  0.00
ATOM   2136  OE2 GLU A 751      17.033  15.143  63.401  1.00  0.00
ATOM   2137  C   GLU A 751      18.728  17.681  59.613  1.00  0.00
ATOM   2138  O   GLU A 751      19.938  17.437  59.505  1.00  0.00
ATOM   2139  N   MET A 752      18.259  18.788  60.168  1.00  0.00
ATOM   2141  CA  MET A 752      19.114  19.968  60.399  1.00  0.00
ATOM   2142  CB  MET A 752      18.222  21.088  60.916  1.00  0.00
ATOM   2143  CG  MET A 752      17.132  21.422  59.904  1.00  0.00
ATOM   2144  SD  MET A 752      15.961  22.698  60.419  1.00  0.00
ATOM   2145  CE  MET A 752      15.283  21.876  61.879  1.00  0.00
ATOM   2146  C   MET A 752      20.269  19.758  61.379  1.00  0.00
ATOM   2147  O   MET A 752      21.357  20.290  61.125  1.00  0.00
ATOM   2148  N   LEU A 753      20.133  18.792  62.277  1.00  0.00
ATOM   2150  CA  LEU A 753      21.222  18.440  63.198  1.00  0.00
ATOM   2151  CB  LEU A 753      20.765  17.356  64.185  1.00  0.00
ATOM   2152  CG  LEU A 753      19.913  17.851  65.360  1.00  0.00
ATOM   2153  CD1 LEU A 753      18.445  18.058  64.991  1.00  0.00
ATOM   2154  CD2 LEU A 753      19.987  16.848  66.506  1.00  0.00
ATOM   2155  C   LEU A 753      22.425  17.898  62.427  1.00  0.00
ATOM   2156  O   LEU A 753      23.505  18.500  62.473  1.00  0.00
ATOM   2157  N   ALA A 754      22.143  17.013  61.485  1.00  0.00
ATOM   2159  CA  ALA A 754      23.213  16.380  60.719  1.00  0.00
ATOM   2160  CB  ALA A 754      22.696  15.058  60.163  1.00  0.00
ATOM   2161  C   ALA A 754      23.677  17.276  59.578  1.00  0.00
ATOM   2162  O   ALA A 754      24.878  17.302  59.286  1.00  0.00
ATOM   2163  N   GLU A 755      22.814  18.182  59.145  1.00  0.00
ATOM   2165  CA  GLU A 755      23.193  19.116  58.085  1.00  0.00
ATOM   2166  CB  GLU A 755      21.960  19.852  57.575  1.00  0.00
ATOM   2167  CG  GLU A 755      21.023  18.913  56.829  1.00  0.00
ATOM   2168  CD  GLU A 755      19.798  19.674  56.332  1.00  0.00
ATOM   2169  OE1 GLU A 755      18.961  20.000  57.165  1.00  0.00
ATOM   2170  OE2 GLU A 755      19.799  20.053  55.169  1.00  0.00
ATOM   2171  C   GLU A 755      24.214  20.130  58.576  1.00  0.00
ATOM   2172  O   GLU A 755      25.291  20.222  57.973  1.00  0.00
ATOM   2173  N   ILE A 756      24.028  20.653  59.779  1.00  0.00
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ATOM	2175	CA	ILE	A	756	24.983	21.654	60.260	1.00	0.00
ATOM	2176	CB	ILE	A	756	24.322	22.545	61.318	1.00	0.00
ATOM	2177	CG2	ILE	A	756	23.817	21.752	62.519	1.00	0.00
ATOM	2178	CG1	ILE	A	756	25.268	23.650	61.779	1.00	0.00
ATOM	2179	CD1	ILE	A	756	25.661	24.571	60.627	1.00	0.00
ATOM	2180	C	ILE	A	756	26.272	21.011	60.780	1.00	0.00
ATOM	2181	O	ILE	A	756	27.349	21.570	60.541	1.00	0.00
ATOM	2182	N	ILE	A	757	26.217	19.749	61.176	1.00	0.00
ATOM	2184	CA	ILE	A	757	27.444	19.091	61.625	1.00	0.00
ATOM	2185	CB	ILE	A	757	27.065	17.921	62.521	1.00	0.00
ATOM	2186	CG2	ILE	A	757	28.286	17.096	62.897	1.00	0.00
ATOM	2187	CG1	ILE	A	757	26.378	18.436	63.778	1.00	0.00
ATOM	2188	CD1	ILE	A	757	25.992	17.291	64.706	1.00	0.00
ATOM	2189	C	ILE	A	757	28.295	18.633	60.441	1.00	0.00
ATOM	2190	O	ILE	A	757	29.513	18.862	60.459	1.00	0.00
ATOM	2191	N	THR	A	758	27.641	18.331	59.328	1.00	0.00
ATOM	2193	CA	THR	A	758	28.359	17.931	58.112	1.00	0.00
ATOM	2194	CB	THR	A	758	27.449	17.028	57.282	1.00	0.00
ATOM	2195	OG1	THR	A	758	27.057	15.934	58.101	1.00	0.00
ATOM	2196	CG2	THR	A	758	28.160	16.456	56.060	1.00	0.00
ATOM	2197	C	THR	A	758	28.812	19.148	57.299	1.00	0.00
ATOM	2198	O	THR	A	758	29.766	19.061	56.517	1.00	0.00
ATOM	2199	N	ASN	A	759	28.256	20.302	57.631	1.00	0.00
ATOM	2201	CA	ASN	A	759	28.694	21.564	57.032	1.00	0.00
ATOM	2202	CB	ASN	A	759	27.521	22.538	57.142	1.00	0.00
ATOM	2203	CG	ASN	A	759	27.446	23.525	55.975	1.00	0.00
ATOM	2204	OD1	ASN	A	759	26.357	23.772	55.443	1.00	0.00
ATOM	2205	ND2	ASN	A	759	28.582	24.076	55.582	1.00	0.00
ATOM	2208	C	ASN	A	759	29.900	22.120	57.796	1.00	0.00
ATOM	2209	O	ASN	A	759	30.681	22.906	57.241	1.00	0.00
ATOM	2210	N	GLN	A	760	30.106	21.637	59.008	1.00	0.00
ATOM	2212	CA	GLN	A	760	31.236	22.099	59.810	1.00	0.00
ATOM	2213	CB	GLN	A	760	30.869	22.018	61.291	1.00	0.00
ATOM	2214	CG	GLN	A	760	29.783	23.005	61.703	1.00	0.00
ATOM	2215	CD	GLN	A	760	30.279	24.443	61.609	1.00	0.00
ATOM	2216	OE1	GLN	A	760	29.595	25.307	61.051	1.00	0.00
ATOM	2217	NE2	GLN	A	760	31.420	24.701	62.228	1.00	0.00
ATOM	2220	C	GLN	A	760	32.486	21.256	59.594	1.00	0.00
ATOM	2221	O	GLN	A	760	33.313	21.514	58.711	1.00	0.00
ATOM	2222	N	ILE	A	761	32.583	20.215	60.399	1.00	0.00
ATOM	2224	CA	ILE	A	761	33.856	19.496	60.557	1.00	0.00
ATOM	2225	CB	ILE	A	761	33.966	18.975	61.994	1.00	0.00
ATOM	2226	CG2	ILE	A	761	33.612	20.082	62.981	1.00	0.00
ATOM	2227	CG1	ILE	A	761	33.122	17.730	62.279	1.00	0.00

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ATOM   2228  CD1 ILE A 761      31.655  18.019  62.571  1.00  0.00
ATOM   2229  C   ILE A 761      34.255  18.353  59.592  1.00  0.00
ATOM   2230  O   ILE A 761      35.470  18.128  59.556  1.00  0.00
ATOM   2231  N   PRO A 762      33.423  17.684  58.786  1.00  0.00
ATOM   2232  CA  PRO A 762      33.990  16.587  57.981  1.00  0.00
ATOM   2233  CB  PRO A 762      32.826  15.811  57.454  1.00  0.00
ATOM   2234  CG  PRO A 762      31.549  16.541  57.811  1.00  0.00
ATOM   2235  CD  PRO A 762      31.969  17.768  58.599  1.00  0.00
ATOM   2236  C   PRO A 762      34.895  17.045  56.832  1.00  0.00
ATOM   2237  O   PRO A 762      35.794  16.284  56.452  1.00  0.00
ATOM   2238  N   LYS A 763      34.858  18.322  56.481  1.00  0.00
ATOM   2240  CA  LYS A 763      35.800  18.836  55.488  1.00  0.00
ATOM   2241  CB  LYS A 763      35.284  20.178  54.987  1.00  0.00
ATOM   2242  CG  LYS A 763      36.216  20.769  53.937  1.00  0.00
ATOM   2243  CD  LYS A 763      35.715  22.129  53.471  1.00  0.00
ATOM   2244  CE  LYS A 763      35.608  23.099  54.641  1.00  0.00
ATOM   2245  NZ  LYS A 763      35.122  24.413  54.193  1.00  0.00
ATOM   2246  C   LYS A 763      37.186  19.017  56.108  1.00  0.00
ATOM   2247  O   LYS A 763      38.180  18.599  55.500  1.00  0.00
ATOM   2248  N   TYR A 764      37.208  19.290  57.403  1.00  0.00
ATOM   2250  CA  TYR A 764      38.473  19.445  58.126  1.00  0.00
ATOM   2251  CB  TYR A 764      38.246  20.377  59.309  1.00  0.00
ATOM   2252  CG  TYR A 764      37.765  21.762  58.892  1.00  0.00
ATOM   2253  CD1 TYR A 764      38.571  22.563  58.091  1.00  0.00
ATOM   2254  CE1 TYR A 764      38.132  23.822  57.703  1.00  0.00
ATOM   2255  CZ  TYR A 764      36.887  24.275  58.118  1.00  0.00
ATOM   2256  OH  TYR A 764      36.439  25.514  57.714  1.00  0.00
ATOM   2257  CE2 TYR A 764      36.081  23.479  58.921  1.00  0.00
ATOM   2258  CD2 TYR A 764      36.521  22.221  59.308  1.00  0.00
ATOM   2259  C   TYR A 764      39.005  18.100  58.610  1.00  0.00
ATOM   2260  O   TYR A 764      40.201  17.963  58.894  1.00  0.00
ATOM   2261  N   SER A 765      38.160  17.085  58.583  1.00  0.00
ATOM   2263  CA  SER A 765      38.642  15.731  58.841  1.00  0.00
ATOM   2264  CB  SER A 765      37.476  14.854  59.262  1.00  0.00
ATOM   2265  OG  SER A 765      37.996  13.542  59.423  1.00  0.00
ATOM   2266  C   SER A 765      39.243  15.129  57.583  1.00  0.00
ATOM   2267  O   SER A 765      40.322  14.528  57.647  1.00  0.00
ATOM   2268  N   ASN A 766      38.692  15.522  56.446  1.00  0.00
ATOM   2270  CA  ASN A 766      39.144  15.001  55.156  1.00  0.00
ATOM   2271  CB  ASN A 766      37.997  15.175  54.170  1.00  0.00
ATOM   2272  CG  ASN A 766      37.991  14.009  53.192  1.00  0.00
ATOM   2273  OD1 ASN A 766      38.705  13.017  53.392  1.00  0.00
ATOM   2274  ND2 ASN A 766      37.139  14.107  52.187  1.00  0.00
ATOM   2277  C   ASN A 766      40.386  15.734  54.649  1.00  0.00
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ATOM	2278	O	ASN	A	766	41.107	15.219	53.788	1.00	0.00
ATOM	2279	N	GLY	A	767	40.683	16.872	55.256	1.00	0.00
ATOM	2281	CA	GLY	A	767	41.940	17.575	54.985	1.00	0.00
ATOM	2282	C	GLY	A	767	42.836	17.626	56.225	1.00	0.00
ATOM	2283	O	GLY	A	767	43.666	18.537	56.347	1.00	0.00
ATOM	2284	N	ASN	A	768	42.705	16.611	57.075	1.00	0.00
ATOM	2286	CA	ASN	A	768	43.451	16.447	58.347	1.00	0.00
ATOM	2287	CB	ASN	A	768	44.624	15.474	58.159	1.00	0.00
ATOM	2288	CG	ASN	A	768	45.422	15.672	56.865	1.00	0.00
ATOM	2289	OD1	ASN	A	768	45.237	14.929	55.895	1.00	0.00
ATOM	2290	ND2	ASN	A	768	46.277	16.679	56.856	1.00	0.00
ATOM	2293	C	ASN	A	768	43.890	17.736	59.057	1.00	0.00
ATOM	2294	O	ASN	A	768	45.074	18.098	59.107	1.00	0.00
ATOM	2295	N	ILE	A	769	42.901	18.422	59.604	1.00	0.00
ATOM	2297	CA	ILE	A	769	43.129	19.606	60.441	1.00	0.00
ATOM	2298	CB	ILE	A	769	42.150	20.697	59.998	1.00	0.00
ATOM	2299	CG2	ILE	A	769	42.373	21.997	60.764	1.00	0.00
ATOM	2300	CG1	ILE	A	769	42.273	20.969	58.501	1.00	0.00
ATOM	2301	CD1	ILE	A	769	43.632	21.569	58.146	1.00	0.00
ATOM	2302	C	ILE	A	769	42.904	19.214	61.905	1.00	0.00
ATOM	2303	O	ILE	A	769	43.157	19.978	62.848	1.00	0.00
ATOM	2304	N	LYS	A	770	42.384	18.009	62.067	1.00	0.00
ATOM	2306	CA	LYS	A	770	42.197	17.426	63.396	1.00	0.00
ATOM	2307	CB	LYS	A	770	40.980	16.514	63.367	1.00	0.00
ATOM	2308	CG	LYS	A	770	39.732	17.226	62.870	1.00	0.00
ATOM	2309	CD	LYS	A	770	38.559	16.256	62.860	1.00	0.00
ATOM	2310	CE	LYS	A	770	37.295	16.905	62.317	1.00	0.00
ATOM	2311	NZ	LYS	A	770	36.176	15.951	62.360	1.00	0.00
ATOM	2312	C	LYS	A	770	43.402	16.583	63.790	1.00	0.00
ATOM	2313	O	LYS	A	770	43.904	15.779	62.995	1.00	0.00
ATOM	2314	N	LYS	A	771	43.789	16.704	65.044	1.00	0.00
ATOM	2316	CA	LYS	A	771	44.871	15.890	65.589	1.00	0.00
ATOM	2317	CB	LYS	A	771	45.718	16.747	66.522	1.00	0.00
ATOM	2318	CG	LYS	A	771	46.919	15.970	67.046	1.00	0.00
ATOM	2319	CD	LYS	A	771	47.746	16.808	68.012	1.00	0.00
ATOM	2320	CE	LYS	A	771	48.978	16.044	68.482	1.00	0.00
ATOM	2321	NZ	LYS	A	771	48.595	14.773	69.117	1.00	0.00
ATOM	2322	C	LYS	A	771	44.279	14.701	66.341	1.00	0.00
ATOM	2323	O	LYS	A	771	43.718	14.839	67.439	1.00	0.00
ATOM	2324	N	LEU	A	772	44.328	13.556	65.681	1.00	0.00
ATOM	2326	CA	LEU	A	772	43.820	12.312	66.269	1.00	0.00
ATOM	2327	CB	LEU	A	772	43.750	11.239	65.190	1.00	0.00
ATOM	2328	CG	LEU	A	772	42.857	11.660	64.027	1.00	0.00
ATOM	2329	CD1	LEU	A	772	42.936	10.647	62.891	1.00	0.00

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ATOM   2330  CD2 LEU A 772      41.412  11.858  64.474  1.00  0.00
ATOM   2331  C   LEU A 772      44.735  11.847  67.392  1.00  0.00
ATOM   2332  O   LEU A 772      45.962  11.777  67.243  1.00  0.00
ATOM   2333  N   LEU A 773      44.121  11.518  68.511  1.00  0.00
ATOM   2335  CA  LEU A 773      44.879  11.136  69.702  1.00  0.00
ATOM   2336  CB  LEU A 773      44.153  11.686  70.918  1.00  0.00
ATOM   2337  CG  LEU A 773      44.107  13.209  70.874  1.00  0.00
ATOM   2338  CD1 LEU A 773      43.185  13.758  71.949  1.00  0.00
ATOM   2339  CD2 LEU A 773      45.502  13.813  71.000  1.00  0.00
ATOM   2340  C   LEU A 773      45.049   9.627  69.811  1.00  0.00
ATOM   2341  O   LEU A 773      44.270   8.925  70.468  1.00  0.00
ATOM   2342  N   PHE A 774      46.102   9.152  69.171  1.00  0.00
ATOM   2344  CA  PHE A 774      46.446   7.730  69.206  1.00  0.00
ATOM   2345  CB  PHE A 774      47.402   7.415  68.061  1.00  0.00
ATOM   2346  CG  PHE A 774      46.818   7.588  66.661  1.00  0.00
ATOM   2347  CD1 PHE A 774      46.000   6.601  66.129  1.00  0.00
ATOM   2348  CE1 PHE A 774      45.469   6.750  64.855  1.00  0.00
ATOM   2349  CZ  PHE A 774      45.756   7.886  64.111  1.00  0.00
ATOM   2350  CE2 PHE A 774      46.580   8.872  64.639  1.00  0.00
ATOM   2351  CD2 PHE A 774      47.113   8.722  65.913  1.00  0.00
ATOM   2352  C   PHE A 774      47.098   7.359  70.533  1.00  0.00
ATOM   2353  O   PHE A 774      47.703   8.196  71.214  1.00  0.00
ATOM   2354  N   HIS A 775      46.872   6.123  70.935  1.00  0.00
ATOM   2356  CA  HIS A 775      47.477   5.606  72.164  1.00  0.00
ATOM   2357  CB  HIS A 775      46.495   4.641  72.813  1.00  0.00
ATOM   2358  CG  HIS A 775      45.110   5.223  73.015  1.00  0.00
ATOM   2359  ND1 HIS A 775      44.779   6.249  73.822  1.00  0.00
ATOM   2361  CE1 HIS A 775      43.452   6.474  73.733  1.00  0.00
ATOM   2362  NE2 HIS A 775      42.943   5.584  72.852  1.00  0.00
ATOM   2363  CD2 HIS A 775      43.953   4.808  72.399  1.00  0.00
ATOM   2364  C   HIS A 775      48.783   4.881  71.850  1.00  0.00
ATOM   2365  O   HIS A 775      49.606   4.626  72.738  1.00  0.00
ATOM   2366  N   GLN A 776      48.938   4.524  70.587  1.00  0.00
ATOM   2368  CA  GLN A 776      50.184   3.948  70.082  1.00  0.00
ATOM   2369  CB  GLN A 776      49.907   2.620  69.368  1.00  0.00
ATOM   2370  CG  GLN A 776      49.722   1.423  70.301  1.00  0.00
ATOM   2371  CD  GLN A 776      48.349   1.388  70.971  1.00  0.00
ATOM   2372  OE1 GLN A 776      47.317   1.635  70.338  1.00  0.00
ATOM   2373  NE2 GLN A 776      48.366   1.169  72.273  1.00  0.00
ATOM   2376  C   GLN A 776      50.844   4.920  69.109  1.00  0.00
ATOM   2377  O   GLN A 776      50.191   5.805  68.543  1.00  0.00
ATOM   2378  N   LYS A 777      52.144   4.759  68.938  1.00  0.00
ATOM   2380  CA  LYS A 777      52.889   5.591  67.988  1.00  0.00
ATOM   2381  CB  LYS A 777      54.380   5.448  68.265  1.00  0.00
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ATOM   2382  CG  LYS A 777      55.198   6.329  67.324  1.00  0.00
ATOM   2383  CD  LYS A 777      56.692   6.164  67.572  1.00  0.00
ATOM   2384  CE  LYS A 777      57.512   7.038  66.629  1.00  0.00
ATOM   2385  NZ  LYS A 777      58.955   6.873  66.868  1.00  0.00
ATOM   2386  C   LYS A 777      52.585   5.164  66.560  1.00  0.00
ATOM   2387  O   LYS A 777      51.832   5.875  65.904  1.00  0.00
ATOM   2388  OXT LYS A 777      53.080   4.119  66.149  1.00  0.00
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Example 22

Structure Coordinates of Site II in Various NHRs, Table III

Below is Table III, which gives the structure coordinates for Site II in various NHRs based on the consensus alignments in Figure 2. The format used is based on that commonly used in the RCSB (Research Collaboratory for Structural Bioinformatics, pdb file format), and the fields listed from left to right are defined as follows: record name, atom serial number, atom name, residue name, chain identifier, residue sequence number, orthogonal coordinate for x in Ångstroms, orthogonal cordinate for y in Ångstroms, orthogonal coordinate for z in Ångstroms, occupancy, and temperature factor.

Table III

AR Site II Residues (ref. 1E3G.pdb)

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ATOM     73  N   GLU A 678       9.927  12.170  14.764  1.00 34.27
ATOM     74  CA  GLU A 678       9.788  11.576  13.433  1.00 33.68
ATOM     75  C   GLU A 678       8.502  10.791  13.361  1.00 31.24
ATOM     76  O   GLU A 678       7.837  10.730  12.318  1.00 29.04
ATOM     77  CB  GLU A 678      10.972  10.692  13.139  1.00 41.54
ATOM     78  CG  GLU A 678      12.250  11.475  13.231  1.00 62.50
ATOM     79  CD  GLU A 678      13.492  10.632  13.140  1.00 75.90
ATOM     80  OE1 GLU A 678      13.382   9.393  13.275  1.00 81.73
ATOM     81  OE2 GLU A 678      14.581  11.222  12.946  1.00 77.79
ATOM     82  N   ALA A 679       8.118  10.229  14.496  1.00 27.29
ATOM     83  CA  ALA A 679       6.878   9.486  14.561  1.00 31.51
ATOM     84  C   ALA A 679       5.658  10.400  14.416  1.00 37.88
ATOM     85  O   ALA A 679       4.657  10.013  13.784  1.00 39.80
ATOM     86  CB  ALA A 679       6.807   8.699  15.862  1.00 32.16
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ATOM	87	N	ILE	A	680	5.748	11.621	14.958	1.00 36.75
ATOM	88	CA	ILE	A	680	4.623	12.567	14.893	1.00 33.51
ATOM	89	C	ILE	A	680	4.603	13.553	13.732	1.00 29.78
ATOM	90	O	ILE	A	680	3.560	14.137	13.425	1.00 35.01
ATOM	91	CB	ILE	A	680	4.445	13.322	16.204	1.00 36.86
ATOM	92	CG1	ILE	A	680	5.672	14.178	16.493	1.00 39.01
ATOM	93	CG2	ILE	A	680	4.222	12.324	17.343	1.00 34.87
ATOM	94	CD1	ILE	A	680	5.503	15.046	17.719	1.00 38.54
ATOM	95	N	GLU	A	681	5.732	13.677	13.044	1.00 31.29
ATOM	96	CA	GLU	A	681	5.833	14.570	11.904	1.00 36.50
ATOM	97	C	GLU	A	681	4.638	14.373	11.013	1.00 38.74
ATOM	98	O	GLU	A	681	4.348	13.251	10.596	1.00 46.06
ATOM	99	CB	GLU	A	681	7.101	14.285	11.106	1.00 33.49
ATOM	100	CG	GLU	A	681	7.361	15.322	10.028	1.00 41.42
ATOM	101	CD	GLU	A	681	7.500	16.742	10.581	1.00 49.46
ATOM	102	OE1	GLU	A	681	7.569	16.924	11.824	1.00 44.22
ATOM	103	OE2	GLU	A	681	7.527	17.687	9.759	1.00 52.12
ATOM	104	N	PRO	A	682	3.892	15.446	10.751	1.00 41.06
ATOM	105	CA	PRO	A	682	2.695	15.422	9.904	1.00 41.12
ATOM	106	C	PRO	A	682	2.968	14.980	8.444	1.00 44.28
ATOM	107	O	PRO	A	682	4.076	15.133	7.920	1.00 36.92
ATOM	108	CB	PRO	A	682	2.214	16.870	9.965	1.00 43.30
ATOM	109	CG	PRO	A	682	2.800	17.399	11.250	1.00 38.89
ATOM	110	CD	PRO	A	682	4.159	16.800	11.261	1.00 39.59
ATOM	111	N	GLY	A	683	1.943	14.446	7.788	1.00 48.21
ATOM	112	CA	GLY	A	683	2.103	13.990	6.416	1.00 51.13
ATOM	113	C	GLY	A	683	1.905	15.043	5.334	1.00 54.68
ATOM	114	O	GLY	A	683	1.817	16.226	5.629	1.00 63.53
ATOM	115	N	VAL	A	684	1.729	14.601	4.089	1.00 57.20
ATOM	116	CA	VAL	A	684	1.544	15.505	2.959	1.00 54.91
ATOM	117	C	VAL	A	684	0.123	16.048	2.952	1.00 54.45
ATOM	118	O	VAL	A	684	-0.828	15.287	2.775	1.00 57.51
ATOM	119	CB	VAL	A	684	1.805	14.792	1.625	1.00 51.72
ATOM	120	CG1	VAL	A	684	1.618	15.769	0.487	1.00 53.17
ATOM	121	CG2	VAL	A	684	3.222	14.212	1.591	1.00 53.92
ATOM	282	N	LEU	A	707	-5.307	26.167	2.636	1.00 38.31
ATOM	283	CA	LEU	A	707	-4.152	25.342	2.982	1.00 37.96
ATOM	284	C	LEU	A	707	-3.767	25.654	4.431	1.00 44.27
ATOM	285	O	LEU	A	707	-3.464	24.747	5.211	1.00 51.41
ATOM	286	CB	LEU	A	707	-2.958	25.608	2.046	1.00 35.41

ATOM	287	CG	LEU	A	707	-1.651	24.872	2.392	1.00 35.71
ATOM	288	CD1	LEU	A	707	-1.895	23.385	2.326	1.00 38.82
ATOM	289	CD2	LEU	A	707	-0.518	25.239	1.459	1.00 33.25
ATOM	290	N	GLY	A	708	-3.782	26.938	4.787	1.00 45.88
ATOM	291	CA	GLY	A	708	-3.463	27.344	6.144	1.00 40.92
ATOM	292	C	GLY	A	708	-4.386	26.618	7.096	1.00 39.05
ATOM	293	O	GLY	A	708	-3.937	25.851	7.924	1.00 45.81
ATOM	314	N	GLN	A	711	-3.596	22.939	7.556	1.00 40.11
ATOM	315	CA	GLN	A	711	-2.310	22.685	8.189	1.00 34.69
ATOM	316	C	GLN	A	711	-2.355	23.007	9.653	1.00 36.60
ATOM	317	O	GLN	A	711	-1.501	22.557	10.408	1.00 40.79
ATOM	318	CB	GLN	A	711	-1.194	23.478	7.542	1.00 42.15
ATOM	319	CG	GLN	A	711	-0.753	22.877	6.244	1.00 43.03
ATOM	320	CD	GLN	A	711	0.553	23.442	5.779	1.00 44.24
ATOM	321	OE1	GLN	A	711	1.321	23.988	6.567	1.00 54.32
ATOM	322	NE2	GLN	A	711	0.828	23.305	4.496	1.00 52.33
ATOM	323	N	LEU	A	712	-3.361	23.778	10.054	1.00 41.25
ATOM	324	CA	LEU	A	712	-3.561	24.163	11.457	1.00 43.47
ATOM	325	C	LEU	A	712	-4.061	22.938	12.222	1.00 45.20
ATOM	326	O	LEU	A	712	-3.595	22.628	13.320	1.00 46.51
ATOM	327	CB	LEU	A	712	-4.585	25.295	11.550	1.00 42.08
ATOM	328	CG	LEU	A	712	-4.829	25.943	12.905	1.00 45.04
ATOM	329	CD1	LEU	A	712	-3.489	26.199	13.594	1.00 48.18
ATOM	330	CD2	LEU	A	712	-5.610	27.248	12.711	1.00 44.32
ATOM	331	N	VAL	A	713	-5.014	22.240	11.623	1.00 42.76
ATOM	332	CA	VAL	A	713	-5.555	21.026	12.198	1.00 41.99
ATOM	333	C	VAL	A	713	-4.383	20.100	12.562	1.00 45.10
ATOM	334	O	VAL	A	713	-4.275	19.646	13.703	1.00 45.64
ATOM	335	CB	VAL	A	713	-6.480	20.348	11.170	1.00 43.85
ATOM	336	CG1	VAL	A	713	-6.887	18.953	11.628	1.00 52.59
ATOM	337	CG2	VAL	A	713	-7.708	21.203	10.966	1.00 42.38
ATOM	338	N	HIS	A	714	-3.471	19.905	11.604	1.00 46.35
ATOM	339	CA	HIS	A	714	-2.286	19.044	11.767	1.00 45.95
ATOM	340	C	HIS	A	714	-1.379	19.495	12.857	1.00 43.82
ATOM	341	O	HIS	A	714	-0.798	18.674	13.571	1.00 48.61
ATOM	342	CB	HIS	A	714	-1.458	18.971	10.487	1.00 49.61
ATOM	343	CG	HIS	A	714	-1.950	17.947	9.519	1.00 62.09
ATOM	344	ND1	HIS	A	714	-3.157	18.058	8.873	1.00 63.02
ATOM	345	CD2	HIS	A	714	-1.404	16.778	9.108	1.00 64.82
ATOM	346	CE1	HIS	A	714	-3.340	17.005	8.100	1.00 70.96

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ATOM    347  NE2 HIS A 714      -2.291  16.211   8.219  1.00 70.54
ATOM    348  N   VAL A 715      -1.172  20.803  12.898  1.00 40.29
ATOM    349  CA  VAL A 715      -0.326  21.415  13.908  1.00 39.63
ATOM    350  C   VAL A 715      -0.962  21.201  15.273  1.00 36.62
ATOM    351  O   VAL A 715      -0.266  20.874  16.244  1.00 30.18
ATOM    352  CB  VAL A 715      -0.101  22.918  13.620  1.00 38.77
ATOM    353  CG1 VAL A 715       0.500  23.617  14.820  1.00 30.17
ATOM    354  CG2 VAL A 715       0.857  23.048  12.463  1.00 40.69
ATOM    355  N   VAL A 716      -2.286  21.329  15.331  1.00 28.64
ATOM    356  CA  VAL A 716      -2.994  21.113  16.570  1.00 28.84
ATOM    357  C   VAL A 716      -2.687  19.683  17.037  1.00 36.83
ATOM    358  O   VAL A 716      -2.078  19.485  18.092  1.00 36.70
ATOM    359  CB  VAL A 716      -4.508  21.331  16.403  1.00 34.61
ATOM    360  CG1 VAL A 716      -5.239  20.839  17.647  1.00 29.84
ATOM    361  CG2 VAL A 716      -4.805  22.811  16.185  1.00 32.32
ATOM    362  N   LYS A 717      -2.972  18.709  16.179  1.00 38.71
ATOM    363  CA  LYS A 717      -2.737  17.313  16.505  1.00 32.14
ATOM    364  C   LYS A 717      -1.263  16.990  16.699  1.00 32.82
ATOM    365  O   LYS A 717      -0.920  16.262  17.631  1.00 34.86
ATOM    366  CB  LYS A 717      -3.370  16.410  15.450  1.00 32.30
ATOM    367  CG  LYS A 717      -4.890  16.352  15.569  1.00 38.88
ATOM    368  CD  LYS A 717      -5.538  15.584  14.436  0.00 36.05
ATOM    369  CE  LYS A 717      -7.009  15.353  14.736  0.00 36.14
ATOM    370  NZ  LYS A 717      -7.739  14.704  13.619  0.00 35.32
ATOM    371  N   TRP A 718      -0.383  17.589  15.893  1.00 31.69
ATOM    372  CA  TRP A 718       1.058  17.319  16.010  1.00 34.84
ATOM    373  C   TRP A 718       1.604  17.753  17.367  1.00 44.15
ATOM    374  O   TRP A 718       2.347  17.014  18.020  1.00 48.94
ATOM    375  CB  TRP A 718       1.850  17.995  14.883  1.00 25.87
ATOM    376  CG  TRP A 718       3.343  18.092  15.136  1.00 25.59
ATOM    377  CD1 TRP A 718       4.279  17.133  14.909  1.00 35.87
ATOM    378  CD2 TRP A 718       4.055  19.232  15.641  1.00 30.45
ATOM    379  NE1 TRP A 718       5.533  17.598  15.237  1.00 32.13
ATOM    380  CE2 TRP A 718       5.419  18.889  15.689  1.00 30.51
ATOM    381  CE3 TRP A 718       3.672  20.519  16.046  1.00 32.20
ATOM    382  CZ2 TRP A 718       6.403  19.782  16.119  1.00 32.90
ATOM    383  CZ3 TRP A 718       4.650  21.408  16.468  1.00 25.41
ATOM    384  CH2 TRP A 718       5.997  21.036  16.503  1.00 28.69
ATOM    552  N   SER A 740       2.351  30.606  17.674  1.00 36.52
ATOM    553  CA  SER A 740       3.459  30.114  16.875  1.00 38.17
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ATOM	554	C	SER	A	740	3.129	29.453	15.535	1.00 38.14
ATOM	555	O	SER	A	740	4.024	29.259	14.706	1.00 41.67
ATOM	556	CB	SER	A	740	4.390	29.231	17.727	1.00 42.37
ATOM	557	OG	SER	A	740	3.756	28.053	18.200	1.00 39.05
ATOM	558	N	TRP	A	741	1.851	29.268	15.236	1.00 32.00
ATOM	559	CA	TRP	A	741	1.482	28.588	14.004	1.00 32.79
ATOM	560	C	TRP	A	741	2.099	29.060	12.681	1.00 34.24
ATOM	561	O	TRP	A	741	2.578	28.250	11.891	1.00 34.43
ATOM	562	CB	TRP	A	741	-0.034	28.446	13.918	1.00 44.21
ATOM	563	CG	TRP	A	741	-0.733	29.487	13.136	1.00 58.12
ATOM	564	CD1	TRP	A	741	-0.889	30.806	13.458	1.00 64.16
ATOM	565	CD2	TRP	A	741	-1.365	29.303	11.870	1.00 63.13
ATOM	566	NE1	TRP	A	741	-1.574	31.462	12.462	1.00 67.31
ATOM	567	CE2	TRP	A	741	-1.882	30.562	11.473	1.00 67.95
ATOM	568	CE3	TRP	A	741	-1.558	28.194	11.031	1.00 57.71
ATOM	569	CZ2	TRP	A	741	-2.561	30.747	10.260	1.00 70.02
ATOM	570	CZ3	TRP	A	741	-2.232	28.373	9.831	1.00 59.16
ATOM	571	CH2	TRP	A	741	-2.731	29.642	9.458	1.00 65.30
ATOM	572	N	MET	A	742	2.184	30.370	12.489	1.00 41.58
ATOM	573	CA	MET	A	742	2.749	30.945	11.265	1.00 39.13
ATOM	574	C	MET	A	742	4.193	30.537	11.090	1.00 30.85
ATOM	575	O	MET	A	742	4.602	30.115	10.017	1.00 34.78
ATOM	576	CB	MET	A	742	2.689	32.476	11.309	1.00 42.39
ATOM	577	CG	MET	A	742	3.147	33.177	10.032	1.00 43.70
ATOM	578	SD	MET	A	742	1.988	32.993	8.658	1.00 45.17
ATOM	579	CE	MET	A	742	0.678	34.132	9.133	1.00 22.14
ATOM	580	N	GLY	A	743	4.954	30.648	12.165	1.00 24.94
ATOM	581	CA	GLY	A	743	6.367	30.312	12.117	1.00 27.24
ATOM	582	C	GLY	A	743	6.630	28.836	11.886	1.00 27.21
ATOM	583	O	GLY	A	743	7.660	28.461	11.322	1.00 27.69
ATOM	584	N	LEU	A	744	5.734	27.983	12.372	1.00 25.91
ATOM	585	CA	LEU	A	744	5.895	26.550	12.172	1.00 26.90
ATOM	586	C	LEU	A	744	5.632	26.287	10.708	1.00 27.04
ATOM	587	O	LEU	A	744	6.375	25.574	10.048	1.00 31.01
ATOM	588	CB	LEU	A	744	4.899	25.755	13.018	1.00 25.72
ATOM	589	CG	LEU	A	744	5.234	25.626	14.514	1.00 29.11
ATOM	590	CD1	LEU	A	744	4.063	25.022	15.275	1.00 23.25
ATOM	591	CD2	LEU	A	744	6.484	24.771	14.689	1.00 24.15
ATOM	592	N	MET	A	745	4.566	26.886	10.200	1.00 25.67
ATOM	593	CA	MET	A	745	4.188	26.725	8.803	1.00 23.96

ATOM	594	C	MET	A	745	5.254	27.179	7.822	1.00 29.61
ATOM	595	O	MET	A	745	5.550	26.480	6.857	1.00 34.60
ATOM	596	CB	MET	A	745	2.895	27.454	8.534	1.00 20.46
ATOM	597	CG	MET	A	745	1.730	26.888	9.310	1.00 19.98
ATOM	598	SD	MET	A	745	0.297	27.272	8.341	1.00 43.15
ATOM	599	CE	MET	A	745	0.642	29.041	8.042	1.00 44.27
ATOM	600	N	VAL	A	746	5.830	28.341	8.095	1.00 27.98
ATOM	601	CA	VAL	A	746	6.876	28.924	7.288	1.00 24.84
ATOM	602	C	VAL	A	746	8.107	28.051	7.345	1.00 28.42
ATOM	603	O	VAL	A	746	8.749	27.786	6.333	1.00 37.05
ATOM	604	CB	VAL	A	746	7.248	30.304	7.835	1.00 31.98
ATOM	605	CG1	VAL	A	746	8.423	30.888	7.073	1.00 29.03
ATOM	606	CG2	VAL	A	746	6.066	31.196	7.737	1.00 32.19
ATOM	607	N	PHE	A	747	8.439	27.607	8.541	1.00 31.29
ATOM	608	CA	PHE	A	747	9.605	26.765	8.736	1.00 32.19
ATOM	609	C	PHE	A	747	9.468	25.401	8.030	1.00 35.99
ATOM	610	O	PHE	A	747	10.398	24.916	7.384	1.00 34.95
ATOM	611	CB	PHE	A	747	9.820	26.536	10.224	1.00 27.90
ATOM	612	CG	PHE	A	747	11.209	26.082	10.573	1.00 26.00
ATOM	613	CD1	PHE	A	747	12.293	26.915	10.343	1.00 24.54
ATOM	614	CD2	PHE	A	747	11.428	24.846	11.166	1.00 27.23
ATOM	615	CE1	PHE	A	747	13.571	26.532	10.699	1.00 25.88
ATOM	616	CE2	PHE	A	747	12.711	24.451	11.528	1.00 25.61
ATOM	617	CZ	PHE	A	747	13.785	25.297	11.293	1.00 28.75
ATOM	618	N	ALA	A	748	8.309	24.774	8.171	1.00 35.11
ATOM	619	CA	ALA	A	748	8.096	23.483	7.561	1.00 34.00
ATOM	620	C	ALA	A	748	8.114	23.683	6.054	1.00 37.26
ATOM	621	O	ALA	A	748	8.831	22.973	5.344	1.00 35.87
ATOM	622	CB	ALA	A	748	6.773	22.896	8.022	1.00 29.48
ATOM	635	N	TRP	A	751	11.304	23.876	4.581	1.00 45.43
ATOM	636	CA	TRP	A	751	11.976	22.588	4.528	1.00 42.53
ATOM	637	C	TRP	A	751	11.519	21.806	3.294	1.00 43.17
ATOM	638	O	TRP	A	751	12.336	21.207	2.596	1.00 40.24
ATOM	639	CB	TRP	A	751	11.717	21.776	5.787	1.00 39.21
ATOM	640	CG	TRP	A	751	12.359	20.401	5.737	1.00 41.85
ATOM	641	CD1	TRP	A	751	11.736	19.213	5.461	1.00 39.44
ATOM	642	CD2	TRP	A	751	13.743	20.085	5.968	1.00 37.37
ATOM	643	NE1	TRP	A	751	12.645	18.186	5.516	1.00 42.23
ATOM	644	CE2	TRP	A	751	13.878	18.692	5.821	1.00 41.26
ATOM	645	CE3	TRP	A	751	14.877	20.841	6.275	1.00 41.35

ATOM	646	CZ2	TRP	A	751	15.110	18.046	5.978	1.00 48.39
ATOM	647	CZ3	TRP	A	751	16.104	20.195	6.431	1.00 39.62
ATOM	648	CH2	TRP	A	751	16.208	18.817	6.280	1.00 43.38
ATOM	649	N	ARG	A	752	10.214	21.792	3.037	1.00 42.27
ATOM	650	CA	ARG	A	752	9.683	21.100	1.862	1.00 41.53
ATOM	651	C	ARG	A	752	10.257	21.740	0.602	1.00 44.18
ATOM	652	O	ARG	A	752	10.522	21.048	-0.380	1.00 43.20
ATOM	653	CB	ARG	A	752	8.163	21.186	1.800	1.00 42.14
ATOM	654	CG	ARG	A	752	7.441	20.465	2.920	1.00 49.76
ATOM	655	CD	ARG	A	752	5.938	20.434	2.649	1.00 48.23
ATOM	656	NE	ARG	A	752	5.382	21.773	2.483	1.00 45.23
ATOM	657	CZ	ARG	A	752	5.013	22.572	3.490	1.00 52.17
ATOM	658	NH1	ARG	A	752	5.131	22.175	4.764	1.00 33.80
ATOM	659	NH2	ARG	A	752	4.536	23.785	3.223	1.00 49.84
ATOM	677	N	THR	A	755	13.948	20.208	0.225	1.00 53.24
ATOM	678	CA	THR	A	755	14.053	18.818	-0.197	1.00 53.33
ATOM	679	C	THR	A	755	13.287	18.474	-1.478	1.00 54.87
ATOM	680	O	THR	A	755	13.554	17.431	-2.068	1.00 57.41
ATOM	681	CB	THR	A	755	13.596	17.830	0.934	1.00 45.98
ATOM	682	OG1	THR	A	755	12.221	18.055	1.245	1.00 49.35
ATOM	683	CG2	THR	A	755	14.405	18.033	2.190	1.00 40.03
ATOM	684	N	ASN	A	756	12.360	19.336	-1.911	1.00 52.97
ATOM	685	CA	ASN	A	756	11.539	19.044	-3.097	1.00 56.15
ATOM	686	C	ASN	A	756	11.821	19.826	-4.394	1.00 55.33
ATOM	687	O	ASN	A	756	11.705	19.257	-5.481	1.00 54.81
ATOM	688	CB	ASN	A	756	10.019	19.124	-2.769	1.00 60.43
ATOM	689	CG	ASN	A	756	9.504	17.959	-1.869	1.00 57.82
ATOM	690	OD1	ASN	A	756	10.123	16.909	-1.763	1.00 55.71
ATOM	691	ND2	ASN	A	756	8.354	18.169	-1.234	1.00 56.46
ATOM	768	N	PRO	A	766	1.766	20.021	-2.533	1.00 52.86
ATOM	769	CA	PRO	A	766	2.120	19.407	-3.813	1.00 50.96
ATOM	770	C	PRO	A	766	1.359	20.040	-4.970	1.00 48.25
ATOM	771	O	PRO	A	766	1.893	20.144	-6.082	1.00 44.31
ATOM	772	CB	PRO	A	766	1.721	17.949	-3.604	1.00 57.00
ATOM	773	CG	PRO	A	766	1.899	17.761	-2.133	1.00 58.08
ATOM	774	CD	PRO	A	766	1.237	19.002	-1.617	1.00 57.23
ATOM	1099	N	PHE	A	804	16.541	19.584	11.932	1.00 32.10
ATOM	1100	CA	PHE	A	804	15.286	20.166	11.519	1.00 26.58
ATOM	1101	C	PHE	A	804	14.157	19.876	12.497	1.00 29.08
ATOM	1102	O	PHE	A	804	13.528	20.793	13.024	1.00 38.23

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ATOM   1103  CB  PHE A 804      14.872  19.663  10.142  1.00 24.46
ATOM   1104  CG  PHE A 804      13.445  20.032   9.767  1.00 35.13
ATOM   1105  CD1 PHE A 804      13.091  21.361   9.540  1.00 36.25
ATOM   1106  CD2 PHE A 804      12.468  19.048   9.617  1.00 38.14
ATOM   1107  CE1 PHE A 804      11.795  21.712   9.164  1.00 27.83
ATOM   1108  CE2 PHE A 804      11.163  19.385   9.238  1.00 39.32
ATOM   1109  CZ  PHE A 804      10.826  20.723   9.011  1.00 38.61
ATOM   1110  N   LEU A 805      13.887  18.600  12.728  1.00 30.73
ATOM   1111  CA  LEU A 805      12.784  18.215  13.586  1.00 28.43
ATOM   1112  C   LEU A 805      12.880  18.799  14.946  1.00 26.10
ATOM   1113  O   LEU A 805      11.881  19.243  15.493  1.00 34.14
ATOM   1114  CB  LEU A 805      12.648  16.702  13.661  1.00 34.10
ATOM   1115  CG  LEU A 805      12.000  16.079  12.423  1.00 43.20
ATOM   1116  CD1 LEU A 805      12.046  14.617  12.600  1.00 36.94
ATOM   1117  CD2 LEU A 805      10.549  16.523  12.252  1.00 44.97
ATOM   1132  N   LYS A 808      12.006  22.545  14.617  1.00 27.59
ATOM   1133  CA  LYS A 808      10.597  22.787  14.378  1.00 27.15
ATOM   1134  C   LYS A 808       9.841  22.681  15.686  1.00 29.83
ATOM   1135  O   LYS A 808       8.954  23.486  15.952  1.00 35.67
ATOM   1136  CB  LYS A 808      10.029  21.837  13.313  1.00 24.49
ATOM   1137  CG  LYS A 808       8.598  22.158  12.811  1.00 23.62
ATOM   1138  CD  LYS A 808       8.148  21.143  11.740  1.00 24.64
ATOM   1139  CE  LYS A 808       7.157  20.101  12.280  1.00 29.39
ATOM   1140  NZ  LYS A 808       5.683  20.529  12.198  1.00 36.92
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ERalpha Site II Residues (ref. 1A52.pdb)

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ATOM     99  N   LEU A 320      99.203  35.236 105.992  1.00 52.59
ATOM    100  CA  LEU A 320     100.556  35.138 106.514  1.00 52.15
ATOM    101  C   LEU A 320     100.597  34.433 107.854  1.00 52.92
ATOM    102  O   LEU A 320     101.488  33.625 108.100  1.00 53.52
ATOM    103  CB  LEU A 320     101.202  36.518 106.612  1.00 51.20
ATOM    104  CG  LEU A 320     101.704  37.051 105.270  1.00 50.53
ATOM    105  CD1 LEU A 320     102.077  38.500 105.353  1.00 50.26
ATOM    106  CD2 LEU A 320     102.898  36.232 104.860  1.00 51.08
ATOM    107  N   ASP A 321      99.629  34.697 108.718  1.00 53.43
ATOM    108  CA  ASP A 321      99.645  34.048 110.015  1.00 54.53
ATOM    109  C   ASP A 321      99.250  32.587 109.939  1.00 54.61
ATOM    110  O   ASP A 321      99.661  31.777 110.769  1.00 54.98
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ATOM	111	CB	ASP	A	321	98.731	34.785	110.993	1.00 56.68
ATOM	112	CG	ASP	A	321	99.259	36.183	111.361	1.00 57.98
ATOM	113	OD1	ASP	A	321	100.332	36.589	110.852	1.00 58.21
ATOM	114	OD2	ASP	A	321	98.594	36.878	112.165	1.00 59.27
ATOM	115	N	ALA	A	322	98.460	32.240	108.936	1.00 54.13
ATOM	116	CA	ALA	A	322	98.014	30.865	108.787	1.00 53.35
ATOM	117	C	ALA	A	322	99.151	29.943	108.300	1.00 52.94
ATOM	118	O	ALA	A	322	99.020	28.702	108.340	1.00 52.54
ATOM	119	CB	ALA	A	322	96.825	30.821	107.812	1.00 54.16
ATOM	120	N	GLU	A	323	100.259	30.544	107.850	1.00 52.13
ATOM	121	CA	GLU	A	323	101.393	29.774	107.338	1.00 51.75
ATOM	122	C	GLU	A	323	101.839	28.683	108.270	1.00 52.28
ATOM	123	O	GLU	A	323	102.104	28.912	109.443	1.00 51.95
ATOM	124	CB	GLU	A	323	102.551	30.690	107.007	1.00 51.77
ATOM	125	CG	GLU	A	323	102.353	31.385	105.703	1.00 52.53
ATOM	126	CD	GLU	A	323	102.333	30.394	104.540	1.00 53.56
ATOM	127	OE1	GLU	A	323	103.433	29.960	104.114	1.00 54.59
ATOM	128	OE2	GLU	A	323	101.227	30.031	104.065	1.00 52.74
ATOM	129	N	PRO	A	324	101.964	27.468	107.743	1.00 53.31
ATOM	130	CA	PRO	A	324	102.372	26.301	108.525	1.00 54.25
ATOM	131	C	PRO	A	324	103.845	26.353	108.943	1.00 54.72
ATOM	132	O	PRO	A	324	104.663	27.053	108.319	1.00 54.54
ATOM	133	CB	PRO	A	324	102.068	25.147	107.565	1.00 53.80
ATOM	134	CG	PRO	A	324	102.536	25.776	106.251	1.00 52.98
ATOM	135	CD	PRO	A	324	101.762	27.082	106.335	1.00 53.61
ATOM	136	N	PRO	A	325	104.208	25.577	109.983	1.00 55.14
ATOM	137	CA	PRO	A	325	105.593	25.547	110.469	1.00 54.70
ATOM	138	C	PRO	A	325	106.379	24.848	109.385	1.00 54.48
ATOM	139	O	PRO	A	325	105.787	24.056	108.642	1.00 55.54
ATOM	140	CB	PRO	A	325	105.498	24.655	111.705	1.00 54.34
ATOM	141	CG	PRO	A	325	104.000	24.741	112.096	1.00 55.28
ATOM	142	CD	PRO	A	325	103.384	24.614	110.742	1.00 55.43
ATOM	143	N	ILE	A	326	107.669	25.137	109.238	1.00 53.52
ATOM	144	CA	ILE	A	326	108.431	24.363	108.257	1.00 53.10
ATOM	145	C	ILE	A	326	108.947	23.151	109.046	1.00 53.30
ATOM	146	O	ILE	A	326	109.625	23.300	110.060	1.00 53.12
ATOM	147	CB	ILE	A	326	109.607	25.120	107.663	1.00 52.50
ATOM	148	CG1	ILE	A	326	109.084	26.335	106.902	1.00 52.50
ATOM	149	CG2	ILE	A	326	110.397	24.196	106.754	1.00 50.93
ATOM	150	CD1	ILE	A	326	110.123	27.100	106.106	1.00 52.06

ATOM	335	N	LEU	A	349	107.683	12.917	105.119	1.00 58.44
ATOM	336	CA	LEU	A	349	107.691	14.379	105.202	1.00 56.38
ATOM	337	C	LEU	A	349	106.356	14.884	104.687	1.00 56.04
ATOM	338	O	LEU	A	349	105.738	15.751	105.278	1.00 56.02
ATOM	339	CB	LEU	A	349	108.809	14.943	104.334	1.00 55.75
ATOM	340	CG	LEU	A	349	108.897	16.461	104.251	1.00 55.07
ATOM	341	CD1	LEU	A	349	109.007	16.966	105.652	1.00 55.38
ATOM	342	CD2	LEU	A	349	110.093	16.927	103.420	1.00 54.73
ATOM	343	N	ALA	A	350	105.905	14.318	103.577	1.00 55.56
ATOM	344	CA	ALA	A	350	104.634	14.712	103.008	1.00 55.49
ATOM	345	C	ALA	A	350	103.449	14.347	103.908	1.00 56.16
ATOM	346	O	ALA	A	350	102.596	15.203	104.190	1.00 56.22
ATOM	347	CB	ALA	A	350	104.464	14.076	101.649	1.00 55.28
ATOM	367	N	GLU	A	353	103.417	16.944	106.610	1.00 56.06
ATOM	368	CA	GLU	A	353	103.047	18.295	106.162	1.00 54.56
ATOM	369	C	GLU	A	353	101.569	18.318	105.901	1.00 54.44
ATOM	370	O	GLU	A	353	100.910	19.359	106.000	1.00 53.15
ATOM	371	CB	GLU	A	353	103.727	18.642	104.868	1.00 53.28
ATOM	372	CG	GLU	A	353	105.109	19.058	105.045	1.00 53.60
ATOM	373	CD	GLU	A	353	105.702	19.417	103.747	1.00 54.14
ATOM	374	OE1	GLU	A	353	105.891	18.500	102.923	1.00 53.79
ATOM	375	OE2	GLU	A	353	105.955	20.618	103.544	1.00 55.37
ATOM	376	N	LEU	A	354	101.068	17.136	105.553	1.00 54.59
ATOM	377	CA	LEU	A	354	99.684	16.970	105.247	1.00 55.05
ATOM	378	C	LEU	A	354	98.899	17.390	106.452	1.00 55.83
ATOM	379	O	LEU	A	354	98.064	18.289	106.369	1.00 56.40
ATOM	380	CB	LEU	A	354	99.415	15.525	104.904	1.00 55.25
ATOM	381	CG	LEU	A	354	98.027	15.235	104.327	1.00 55.93
ATOM	382	CD1	LEU	A	354	97.723	16.127	103.112	1.00 55.51
ATOM	383	CD2	LEU	A	354	98.005	13.772	103.920	1.00 56.20
ATOM	384	N	VAL	A	355	99.198	16.758	107.584	1.00 56.64
ATOM	385	CA	VAL	A	355	98.517	17.047	108.854	1.00 56.37
ATOM	386	C	VAL	A	355	98.478	18.566	109.086	1.00 56.20
ATOM	387	O	VAL	A	355	97.429	19.123	109.399	1.00 55.29
ATOM	388	CB	VAL	A	355	99.243	16.309	110.047	1.00 56.40
ATOM	389	CG1	VAL	A	355	98.476	16.491	111.354	1.00 55.19
ATOM	390	CG2	VAL	A	355	99.383	14.813	109.719	1.00 55.99
ATOM	391	N	HIS	A	356	99.616	19.234	108.914	1.00 56.56
ATOM	392	CA	HIS	A	356	99.668	20.689	109.087	1.00 57.22
ATOM	393	C	HIS	A	356	98.862	21.449	108.039	1.00 57.46

ATOM	394	O	HIS	A	356	98.374	22.554	108.309	1.00 57.24
ATOM	395	CB	HIS	A	356	101.119	21.167	109.071	1.00 57.78
ATOM	396	CG	HIS	A	356	101.864	20.809	110.316	1.00 58.97
ATOM	397	ND1	HIS	A	356	101.689	21.487	111.507	1.00 57.69
ATOM	398	CD2	HIS	A	356	102.697	19.774	110.586	1.00 59.14
ATOM	399	CE1	HIS	A	356	102.381	20.882	112.454	1.00 58.77
ATOM	400	NE2	HIS	A	356	103.001	19.841	111.922	1.00 59.96
ATOM	401	N	MET	A	357	98.730	20.853	106.846	1.00 57.44
ATOM	402	CA	MET	A	357	97.969	21.458	105.766	1.00 56.62
ATOM	403	C	MET	A	357	96.513	21.540	106.169	1.00 57.20
ATOM	404	O	MET	A	357	95.855	22.535	105.872	1.00 57.88
ATOM	405	CB	MET	A	357	98.074	20.644	104.497	1.00 56.36
ATOM	406	CG	MET	A	357	97.404	21.316	103.317	1.00 55.15
ATOM	407	SD	MET	A	357	97.619	20.356	101.830	1.00 54.74
ATOM	408	CE	MET	A	357	99.420	20.228	101.751	1.00 52.92
ATOM	409	N	ILE	A	358	95.995	20.505	106.827	1.00 56.60
ATOM	410	CA	ILE	A	358	94.614	20.556	107.282	1.00 56.75
ATOM	411	C	ILE	A	358	94.424	21.724	108.270	1.00 57.56
ATOM	412	O	ILE	A	358	93.376	22.355	108.292	1.00 57.84
ATOM	413	CB	ILE	A	358	94.217	19.299	108.025	1.00 56.52
ATOM	414	CG1	ILE	A	358	94.325	18.071	107.119	1.00 56.72
ATOM	415	CG2	ILE	A	358	92.819	19.475	108.563	1.00 55.68
ATOM	416	CD1	ILE	A	358	93.270	17.991	106.063	1.00 57.04
ATOM	417	N	ASN	A	359	95.428	22.001	109.102	1.00 58.53
ATOM	418	CA	ASN	A	359	95.328	23.101	110.087	1.00 59.39
ATOM	419	C	ASN	A	359	95.343	24.434	109.366	1.00 59.28
ATOM	420	O	ASN	A	359	94.671	25.393	109.757	1.00 59.79
ATOM	421	CB	ASN	A	359	96.503	23.094	111.093	1.00 59.23
ATOM	422	CG	ASN	A	359	96.406	21.977	112.137	1.00 58.85
ATOM	423	OD1	ASN	A	359	97.357	21.766	112.883	1.00 58.21
ATOM	424	ND2	ASN	A	359	95.259	21.280	112.207	1.00 58.60
ATOM	425	N	TRP	A	360	96.143	24.485	108.316	1.00 59.09
ATOM	426	CA	TRP	A	360	96.273	25.691	107.511	1.00 58.86
ATOM	427	C	TRP	A	360	94.979	25.972	106.752	1.00 59.22
ATOM	428	O	TRP	A	360	94.404	27.049	106.907	1.00 59.55
ATOM	429	CB	TRP	A	360	97.433	25.524	106.539	1.00 57.75
ATOM	430	CG	TRP	A	360	97.432	26.496	105.428	1.00 55.96
ATOM	431	CD1	TRP	A	360	97.898	27.775	105.448	1.00 55.46
ATOM	432	CD2	TRP	A	360	96.932	26.269	104.117	1.00 54.62
ATOM	433	NE1	TRP	A	360	97.723	28.360	104.223	1.00 53.87

ATOM	434	CE2	TRP	A	360	97.128	27.456	103.387	1.00	53.93
ATOM	435	CE3	TRP	A	360	96.336	25.172	103.486	1.00	54.51
ATOM	436	CZ2	TRP	A	360	96.751	27.583	102.062	1.00	54.47
ATOM	437	CZ3	TRP	A	360	95.956	25.293	102.159	1.00	54.55
ATOM	438	CH2	TRP	A	360	96.164	26.491	101.461	1.00	55.14
ATOM	606	N	ALA	A	382	93.720	19.091	95.631	1.00	48.18
ATOM	607	CA	ALA	A	382	94.850	20.021	95.659	1.00	46.44
ATOM	608	C	ALA	A	382	96.066	19.788	96.546	1.00	45.10
ATOM	609	O	ALA	A	382	97.059	20.502	96.421	1.00	44.69
ATOM	610	CB	ALA	A	382	94.313	21.418	95.944	1.00	46.52
ATOM	611	N	TRP	A	383	96.023	18.796	97.417	1.00	43.80
ATOM	612	CA	TRP	A	383	97.132	18.602	98.333	1.00	42.62
ATOM	613	C	TRP	A	383	98.512	18.580	97.713	1.00	42.80
ATOM	614	O	TRP	A	383	99.418	19.269	98.192	1.00	42.64
ATOM	615	CB	TRP	A	383	96.935	17.356	99.180	1.00	41.81
ATOM	616	CG	TRP	A	383	97.078	16.095	98.441	1.00	42.13
ATOM	617	CD1	TRP	A	383	96.121	15.443	97.699	1.00	41.98
ATOM	618	CD2	TRP	A	383	98.280	15.329	98.310	1.00	42.10
ATOM	619	NE1	TRP	A	383	96.664	14.313	97.114	1.00	41.37
ATOM	620	CE2	TRP	A	383	97.984	14.219	97.472	1.00	41.64
ATOM	621	CE3	TRP	A	383	99.582	15.472	98.815	1.00	41.02
ATOM	622	CZ2	TRP	A	383	98.942	13.264	97.132	1.00	41.39
ATOM	623	CZ3	TRP	A	383	100.529	14.525	98.475	1.00	40.98
ATOM	624	CH2	TRP	A	383	100.205	13.430	97.639	1.00	41.01
ATOM	625	N	LEU	A	384	98.700	17.823	96.644	1.00	42.54
ATOM	626	CA	LEU	A	384	100.031	17.787	96.049	1.00	42.84
ATOM	627	C	LEU	A	384	100.438	19.088	95.346	1.00	43.49
ATOM	628	O	LEU	A	384	101.630	19.377	95.233	1.00	44.08
ATOM	629	CB	LEU	A	384	100.172	16.594	95.094	1.00	41.56
ATOM	630	CG	LEU	A	384	101.523	16.480	94.387	1.00	41.31
ATOM	631	CD1	LEU	A	384	102.679	16.449	95.405	1.00	41.62
ATOM	632	CD2	LEU	A	384	101.520	15.229	93.530	1.00	40.95
ATOM	633	N	GLU	A	385	99.476	19.869	94.842	1.00	44.36
ATOM	634	CA	GLU	A	385	99.859	21.138	94.202	1.00	44.04
ATOM	635	C	GLU	A	385	100.354	21.981	95.349	1.00	43.68
ATOM	636	O	GLU	A	385	101.436	22.569	95.280	1.00	44.08
ATOM	637	CB	GLU	A	385	98.682	21.871	93.532	1.00	44.27
ATOM	638	CG	GLU	A	385	98.129	21.194	92.295	1.00	45.37
ATOM	639	CD	GLU	A	385	97.018	21.989	91.622	1.00	45.49
ATOM	640	OE1	GLU	A	385	97.298	23.003	90.937	1.00	47.13

ATOM	641	OE2	GLU	A	385	95.852	21.600	91.785	1.00	45.12
ATOM	642	N	ILE	A	386	99.566	22.011	96.423	1.00	42.40
ATOM	643	CA	ILE	A	386	99.931	22.805	97.584	1.00	41.27
ATOM	644	C	ILE	A	386	101.317	22.465	98.129	1.00	41.05
ATOM	645	O	ILE	A	386	102.083	23.374	98.426	1.00	41.04
ATOM	646	CB	ILE	A	386	98.857	22.694	98.682	1.00	41.25
ATOM	647	CG1	ILE	A	386	97.560	23.323	98.161	1.00	41.02
ATOM	648	CG2	ILE	A	386	99.318	23.391	99.969	1.00	40.11
ATOM	649	CD1	ILE	A	386	96.406	23.327	99.158	1.00	41.13
ATOM	650	N	LEU	A	387	101.667	21.179	98.251	1.00	40.50
ATOM	651	CA	LEU	A	387	103.012	20.854	98.734	1.00	38.67
ATOM	652	C	LEU	A	387	104.012	21.352	97.729	1.00	37.88
ATOM	653	O	LEU	A	387	104.989	21.978	98.081	1.00	38.53
ATOM	654	CB	LEU	A	387	103.241	19.361	98.888	1.00	38.37
ATOM	655	CG	LEU	A	387	102.483	18.607	99.963	1.00	38.32
ATOM	656	CD1	LEU	A	387	102.980	17.207	99.926	1.00	38.21
ATOM	657	CD2	LEU	A	387	102.688	19.217	101.331	1.00	38.68
ATOM	658	N	MET	A	388	103.767	21.085	96.464	1.00	36.94
ATOM	659	CA	MET	A	388	104.704	21.522	95.468	1.00	37.35
ATOM	660	C	MET	A	388	105.013	23.017	95.449	1.00	37.65
ATOM	661	O	MET	A	388	106.181	23.403	95.272	1.00	37.12
ATOM	662	CB	MET	A	388	104.247	21.039	94.100	1.00	38.12
ATOM	663	CG	MET	A	388	104.336	19.543	94.010	1.00	39.96
ATOM	664	SD	MET	A	388	104.131	18.976	92.374	1.00	43.43
ATOM	665	CE	MET	A	388	104.602	17.301	92.499	1.00	42.19
ATOM	666	N	ILE	A	389	104.000	23.864	95.652	1.00	37.61
ATOM	667	CA	ILE	A	389	104.260	25.297	95.592	1.00	37.05
ATOM	668	C	ILE	A	389	105.089	25.716	96.800	1.00	37.88
ATOM	669	O	ILE	A	389	105.971	26.595	96.702	1.00	36.98
ATOM	670	CB	ILE	A	389	102.953	26.125	95.495	1.00	35.49
ATOM	671	CG1	ILE	A	389	103.300	27.514	94.961	1.00	34.22
ATOM	672	CG2	ILE	A	389	102.285	26.217	96.822	1.00	33.85
ATOM	673	CD1	ILE	A	389	102.156	28.318	94.504	1.00	33.77
ATOM	674	N	GLY	A	390	104.823	25.059	97.933	1.00	38.26
ATOM	675	CA	GLY	A	390	105.579	25.348	99.144	1.00	39.15
ATOM	676	C	GLY	A	390	107.045	24.961	98.905	1.00	39.94
ATOM	677	O	GLY	A	390	107.952	25.778	99.094	1.00	39.41
ATOM	693	N	TRP	A	393	108.644	27.458	96.768	1.00	46.72
ATOM	694	CA	TRP	A	393	108.925	28.703	97.470	1.00	48.60
ATOM	695	C	TRP	A	393	110.211	28.586	98.301	1.00	49.48

ATOM	696	O	TRP	A	393	111.101	29.434	98.214	1.00 49.93
ATOM	697	CB	TRP	A	393	107.737	29.024	98.368	1.00 48.90
ATOM	698	CG	TRP	A	393	107.887	30.184	99.292	1.00 48.84
ATOM	699	CD1	TRP	A	393	107.712	30.170	100.653	1.00 49.55
ATOM	700	CD2	TRP	A	393	108.060	31.550	98.930	1.00 49.05
ATOM	701	NE1	TRP	A	393	107.755	31.455	101.162	1.00 49.29
ATOM	702	CE2	TRP	A	393	107.965	32.321	100.124	1.00 48.99
ATOM	703	CE3	TRP	A	393	108.278	32.208	97.712	1.00 50.02
ATOM	704	CZ2	TRP	A	393	108.082	33.712	100.134	1.00 49.14
ATOM	705	CZ3	TRP	A	393	108.393	33.614	97.718	1.00 50.46
ATOM	706	CH2	TRP	A	393	108.293	34.344	98.927	1.00 49.90
ATOM	707	N	ARG	A	394	110.295	27.531	99.105	1.00 50.21
ATOM	708	CA	ARG	A	394	111.461	27.274	99.960	1.00 50.94
ATOM	709	C	ARG	A	394	112.756	27.068	99.155	1.00 52.04
ATOM	710	O	ARG	A	394	113.844	27.404	99.643	1.00 52.38
ATOM	711	CB	ARG	A	394	111.262	26.006	100.809	1.00 50.31
ATOM	712	CG	ARG	A	394	110.034	25.974	101.674	1.00 50.30
ATOM	713	CD	ARG	A	394	110.153	24.878	102.698	1.00 49.88
ATOM	714	NE	ARG	A	394	109.924	23.537	102.187	1.00 49.74
ATOM	715	CZ	ARG	A	394	108.716	23.038	101.973	1.00 50.74
ATOM	716	NH1	ARG	A	394	107.641	23.780	102.224	1.00 51.52
ATOM	717	NH2	ARG	A	394	108.572	21.792	101.552	1.00 50.41
ATOM	732	N	GLU	A	397	115.749	30.358	97.413	1.00 59.67
ATOM	733	CA	GLU	A	397	117.049	30.786	97.986	1.00 60.86
ATOM	734	C	GLU	A	397	118.156	29.784	97.665	1.00 60.54
ATOM	735	O	GLU	A	397	119.328	30.062	97.922	1.00 61.19
ATOM	736	CB	GLU	A	397	116.974	30.899	99.534	1.00 62.68
ATOM	737	CG	GLU	A	397	116.006	31.953	100.067	1.00 65.83
ATOM	738	CD	GLU	A	397	116.522	33.384	99.863	1.00 67.85
ATOM	739	OE1	GLU	A	397	117.298	33.861	100.728	1.00 68.99
ATOM	740	OE2	GLU	A	397	116.177	34.021	98.830	1.00 68.91
ATOM	803	N	PRO	A	406	114.567	21.882	106.062	1.00 52.84
ATOM	804	CA	PRO	A	406	115.835	22.473	106.457	1.00 53.87
ATOM	805	C	PRO	A	406	116.961	21.462	106.436	1.00 55.27
ATOM	806	O	PRO	A	406	118.046	21.757	105.935	1.00 55.84
ATOM	807	CB	PRO	A	406	115.533	22.985	107.848	1.00 53.50
ATOM	808	CG	PRO	A	406	114.115	23.420	107.694	1.00 53.44
ATOM	809	CD	PRO	A	406	113.558	22.158	107.092	1.00 52.74
ATOM	1112	N	PHE	A	445	102.932	34.883	97.394	1.00 40.62
ATOM	1113	CA	PHE	A	445	102.968	33.433	97.569	1.00 39.52

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ATOM   1114  C   PHE A 445     101.768  32.864  98.288  1.00 39.48
ATOM   1115  O   PHE A 445     101.164  31.903  97.814  1.00 40.17
ATOM   1116  CB  PHE A 445     104.236  33.044  98.341  1.00 38.13
ATOM   1117  CG  PHE A 445     104.251  31.623  98.840  1.00 36.69
ATOM   1118  CD1 PHE A 445     104.293  30.555  97.960  1.00 35.89
ATOM   1119  CD2 PHE A 445     104.261  31.360 100.212  1.00 36.19
ATOM   1120  CE1 PHE A 445     104.350  29.242  98.442  1.00 35.78
ATOM   1121  CE2 PHE A 445     104.319  30.065 100.693  1.00 35.05
ATOM   1122  CZ  PHE A 445     104.364  29.003  99.808  1.00 35.27
ATOM   1123  N   VAL A 446     101.418  33.438  99.430  1.00 39.54
ATOM   1124  CA  VAL A 446     100.298  32.912 100.190  1.00 40.25
ATOM   1125  C   VAL A 446      98.963  33.084  99.460  1.00 41.56
ATOM   1126  O   VAL A 446      98.039  32.272  99.652  1.00 42.13
ATOM   1127  CB  VAL A 446     100.236  33.551 101.578  1.00 39.66
ATOM   1128  CG1 VAL A 446     101.518  33.255 102.312  1.00 39.41
ATOM   1129  CG2 VAL A 446     100.035  35.041 101.452  1.00 39.84
ATOM   1144  N   LYS A 449      98.826  30.117  97.098  1.00 40.49
ATOM   1145  CA  LYS A 449      98.582  28.832  97.766  1.00 40.08
ATOM   1146  C   LYS A 449      97.065  28.707  98.033  1.00 39.21
ATOM   1147  O   LYS A 449      96.463  27.681  97.721  1.00 38.04
ATOM   1148  CB  LYS A 449      99.418  28.783  99.070  1.00 42.46
ATOM   1149  CG  LYS A 449      99.578  27.462  99.940  1.00 42.75
ATOM   1150  CD  LYS A 449     100.593  27.825 101.073  1.00 43.32
ATOM   1151  CE  LYS A 449     100.997  26.726 102.078  1.00 45.38
ATOM   1152  NZ  LYS A 449     100.059  26.334 103.235  1.00 45.31
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ERbeta Site II Residues (ref. 1L2J.pdb)

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ATOM     84  N   LEU A 273      25.561  69.746   8.280  1.00 29.28
ATOM     85  CA  LEU A 273      24.842  68.816   7.428  1.00 30.73
ATOM     86  C   LEU A 273      23.457  69.322   7.107  1.00 32.14
ATOM     87  O   LEU A 273      23.002  69.256   5.967  1.00 31.30
ATOM     88  CB  LEU A 273      24.733  67.449   8.102  1.00 30.00
ATOM     89  CG  LEU A 273      25.927  66.508   7.951  1.00 31.09
ATOM     90  CD1 LEU A 273      25.722  65.262   8.804  1.00 29.29
ATOM     91  CD2 LEU A 273      26.090  66.130   6.472  1.00 33.12
ATOM     92  N   GLU A 274      22.799  69.848   8.130  1.00 34.03
ATOM     93  CA  GLU A 274      21.446  70.334   7.965  1.00 37.36
ATOM     94  C   GLU A 274      21.402  71.743   7.419  1.00 37.99
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ATOM	95	O	GLU	A	274	20.411	72.152	6.825	1.00 38.85
ATOM	96	CB	GLU	A	274	20.712	70.268	9.297	1.00 38.49
ATOM	97	N	ALA	A	275	22.490	72.475	7.606	1.00 38.21
ATOM	98	CA	ALA	A	275	22.562	73.860	7.168	1.00 37.18
ATOM	99	C	ALA	A	275	22.827	73.954	5.675	1.00 36.12
ATOM	100	O	ALA	A	275	22.533	74.959	5.038	1.00 36.11
ATOM	101	CB	ALA	A	275	23.645	74.578	7.943	1.00 35.11
ATOM	102	N	GLU	A	276	23.338	72.873	5.115	1.00 37.82
ATOM	103	CA	GLU	A	276	23.639	72.836	3.691	1.00 40.70
ATOM	104	C	GLU	A	276	22.412	73.106	2.854	1.00 41.89
ATOM	105	O	GLU	A	276	21.405	72.425	2.974	1.00 44.28
ATOM	106	CB	GLU	A	276	24.204	71.470	3.289	1.00 40.51
ATOM	107	CG	GLU	A	276	25.707	71.443	3.107	1.00 41.75
ATOM	108	CD	GLU	A	276	26.158	72.093	1.824	1.00 41.08
ATOM	109	OE1	GLU	A	276	25.914	71.528	0.732	1.00 42.10
ATOM	110	OE2	GLU	A	276	26.762	73.175	1.913	1.00 41.89
ATOM	111	N	PRO	A	277	22.477	74.110	1.991	1.00 43.10
ATOM	112	CA	PRO	A	277	21.323	74.417	1.139	1.00 45.04
ATOM	113	C	PRO	A	277	21.232	73.506	-0.074	1.00 47.07
ATOM	114	O	PRO	A	277	22.234	72.937	-0.494	1.00 48.36
ATOM	115	CB	PRO	A	277	21.573	75.861	0.745	1.00 45.33
ATOM	116	CG	PRO	A	277	23.045	75.885	0.600	1.00 44.31
ATOM	117	CD	PRO	A	277	23.528	75.128	1.822	1.00 43.44
ATOM	118	N	PRO	A	278	20.028	73.356	-0.657	1.00 49.65
ATOM	119	CA	PRO	A	278	19.860	72.488	-1.833	1.00 50.10
ATOM	120	C	PRO	A	278	20.412	73.155	-3.085	1.00 49.50
ATOM	121	O	PRO	A	278	20.314	74.367	-3.246	1.00 49.29
ATOM	122	CB	PRO	A	278	18.346	72.282	-1.908	1.00 51.43
ATOM	123	CG	PRO	A	278	17.870	72.581	-0.487	1.00 51.67
ATOM	124	CD	PRO	A	278	18.715	73.778	-0.141	1.00 50.69
ATOM	125	N	HIS	A	279	20.988	72.360	-3.972	1.00 49.61
ATOM	126	CA	HIS	A	279	21.572	72.901	-5.187	1.00 49.19
ATOM	127	C	HIS	A	279	20.548	73.722	-5.941	1.00 47.98
ATOM	128	O	HIS	A	279	19.384	73.357	-6.022	1.00 46.87
ATOM	129	CB	HIS	A	279	22.109	71.769	-6.070	1.00 48.45
ATOM	235	N	LEU	A	301	23.142	82.321	-11.653	1.00 39.42
ATOM	236	CA	LEU	A	301	23.297	81.248	-10.678	1.00 38.51
ATOM	237	C	LEU	A	301	24.074	81.762	-9.477	1.00 36.22
ATOM	238	O	LEU	A	301	23.680	81.564	-8.335	1.00 35.05
ATOM	239	CB	LEU	A	301	24.040	80.071	-11.309	1.00 41.75

ATOM	240	CG	LEU	A	301	24.287	78.874	-10.391	1.00 43.32
ATOM	241	CD1	LEU	A	301	22.964	78.215	-10.003	1.00 43.90
ATOM	242	CD2	LEU	A	301	25.196	77.887	-11.100	1.00 44.77
ATOM	243	N	ALA	A	302	25.181	82.433	-9.756	1.00 35.01
ATOM	244	CA	ALA	A	302	26.024	82.999	-8.719	1.00 37.36
ATOM	245	C	ALA	A	302	25.196	83.771	-7.705	1.00 38.89
ATOM	246	O	ALA	A	302	25.316	83.560	-6.498	1.00 39.07
ATOM	247	CB	ALA	A	302	27.061	83.915	-9.345	1.00 36.91
ATOM	265	N	GLU	A	305	23.169	81.589	-5.589	1.00 42.82
ATOM	266	CA	GLU	A	305	23.951	80.823	-4.627	1.00 42.67
ATOM	267	C	GLU	A	305	24.482	81.691	-3.495	1.00 41.23
ATOM	268	O	GLU	A	305	24.567	81.235	-2.351	1.00 40.16
ATOM	269	CB	GLU	A	305	25.106	80.126	-5.330	1.00 44.09
ATOM	270	CG	GLU	A	305	24.645	78.970	-6.160	1.00 44.66
ATOM	271	CD	GLU	A	305	25.782	78.274	-6.843	1.00 45.46
ATOM	272	OE1	GLU	A	305	26.524	78.938	-7.599	1.00 43.22
ATOM	273	OE2	GLU	A	305	25.931	77.056	-6.623	1.00 49.46
ATOM	274	N	LEU	A	306	24.840	82.935	-3.816	1.00 38.20
ATOM	275	CA	LEU	A	306	25.341	83.853	-2.810	1.00 36.32
ATOM	276	C	LEU	A	306	24.295	84.071	-1.710	1.00 36.84
ATOM	277	O	LEU	A	306	24.637	84.147	-0.527	1.00 39.11
ATOM	278	CB	LEU	A	306	25.746	85.173	-3.460	1.00 30.89
ATOM	279	CG	LEU	A	306	27.024	85.078	-4.296	1.00 29.12
ATOM	280	CD1	LEU	A	306	27.244	86.344	-5.055	1.00 28.99
ATOM	281	CD2	LEU	A	306	28.213	84.831	-3.411	1.00 31.75
ATOM	282	N	VAL	A	307	23.024	84.144	-2.093	1.00 35.35
ATOM	283	CA	VAL	A	307	21.943	84.325	-1.121	1.00 35.56
ATOM	284	C	VAL	A	307	21.963	83.154	-0.143	1.00 35.53
ATOM	285	O	VAL	A	307	21.982	83.334	1.078	1.00 36.47
ATOM	286	CB	VAL	A	307	20.561	84.367	-1.821	1.00 35.38
ATOM	287	CG1	VAL	A	307	19.464	84.541	-0.812	1.00 35.78
ATOM	288	CG2	VAL	A	307	20.516	85.504	-2.806	1.00 37.25
ATOM	289	N	HIS	A	308	21.954	81.949	-0.699	1.00 35.96
ATOM	290	CA	HIS	A	308	21.996	80.722	0.085	1.00 35.90
ATOM	291	C	HIS	A	308	23.221	80.708	0.983	1.00 32.55
ATOM	292	O	HIS	A	308	23.175	80.248	2.122	1.00 30.70
ATOM	293	CB	HIS	A	308	22.065	79.517	-0.850	1.00 42.30
ATOM	294	CG	HIS	A	308	20.738	79.096	-1.395	1.00 50.05
ATOM	295	ND1	HIS	A	308	19.727	78.607	-0.593	1.00 55.44
ATOM	296	CD2	HIS	A	308	20.253	79.087	-2.659	1.00 52.89

ATOM	297	CE1	HIS	A	308	18.678	78.315	-1.340	1.00	56.67
ATOM	298	NE2	HIS	A	308	18.970	78.597	-2.598	1.00	56.96
ATOM	299	N	MET	A	309	24.323	81.214	0.448	1.00	28.95
ATOM	300	CA	MET	A	309	25.571	81.247	1.178	1.00	27.16
ATOM	301	C	MET	A	309	25.441	82.032	2.469	1.00	24.47
ATOM	302	O	MET	A	309	25.939	81.613	3.503	1.00	24.53
ATOM	303	CB	MET	A	309	26.669	81.852	0.313	1.00	25.50
ATOM	304	CG	MET	A	309	28.026	81.510	0.830	1.00	26.26
ATOM	305	SD	MET	A	309	29.265	82.251	-0.145	1.00	30.35
ATOM	306	CE	MET	A	309	29.366	83.764	0.675	1.00	29.47
ATOM	307	N	ILE	A	310	24.767	83.171	2.404	1.00	19.70
ATOM	308	CA	ILE	A	310	24.577	83.993	3.576	1.00	19.52
ATOM	309	C	ILE	A	310	23.701	83.289	4.623	1.00	21.07
ATOM	310	O	ILE	A	310	23.959	83.390	5.818	1.00	21.03
ATOM	311	CB	ILE	A	310	23.972	85.345	3.169	1.00	18.29
ATOM	312	CG1	ILE	A	310	24.925	86.021	2.176	1.00	16.69
ATOM	313	CG2	ILE	A	310	23.728	86.209	4.403	1.00	16.22
ATOM	314	CD1	ILE	A	310	24.556	87.408	1.758	1.00	17.44
ATOM	315	N	SER	A	311	22.673	82.572	4.176	1.00	21.38
ATOM	316	CA	SER	A	311	21.814	81.838	5.091	1.00	21.32
ATOM	317	C	SER	A	311	22.670	80.769	5.732	1.00	22.38
ATOM	318	O	SER	A	311	22.623	80.552	6.940	1.00	27.93
ATOM	319	CB	SER	A	311	20.668	81.173	4.344	1.00	19.97
ATOM	320	OG	SER	A	311	19.790	82.141	3.825	1.00	29.81
ATOM	321	N	TRP	A	312	23.451	80.103	4.893	1.00	18.68
ATOM	322	CA	TRP	A	312	24.347	79.055	5.328	1.00	16.46
ATOM	323	C	TRP	A	312	25.280	79.582	6.420	1.00	17.03
ATOM	324	O	TRP	A	312	25.408	78.979	7.485	1.00	18.99
ATOM	325	CB	TRP	A	312	25.147	78.551	4.120	1.00	14.40
ATOM	326	CG	TRP	A	312	26.278	77.658	4.485	1.00	12.23
ATOM	327	CD1	TRP	A	312	26.195	76.379	4.934	1.00	11.53
ATOM	328	CD2	TRP	A	312	27.673	77.999	4.478	1.00	12.83
ATOM	329	NE1	TRP	A	312	27.456	75.894	5.222	1.00	15.57
ATOM	330	CE2	TRP	A	312	28.379	76.869	4.955	1.00	13.92
ATOM	331	CE3	TRP	A	312	28.391	79.150	4.137	1.00	11.91
ATOM	332	CZ2	TRP	A	312	29.775	76.856	5.075	1.00	13.72
ATOM	333	CZ3	TRP	A	312	29.790	79.142	4.261	1.00	11.65
ATOM	334	CH2	TRP	A	312	30.460	78.006	4.736	1.00	15.65
ATOM	498	N	CYS	A	334	35.346	85.584	1.011	1.00	10.61
ATOM	499	CA	CYS	A	334	35.360	84.154	0.704	1.00	8.93

ATOM	500	C	CYS	A	334	34.348	83.651	-0.307	1.00 10.23
ATOM	501	O	CYS	A	334	34.330	82.462	-0.629	1.00 6.33
ATOM	502	CB	CYS	A	334	35.138	83.351	1.984	1.00 13.63
ATOM	503	SG	CYS	A	334	33.388	83.352	2.564	1.00 15.47
ATOM	504	N	TRP	A	335	33.494	84.530	-0.802	1.00 11.06
ATOM	505	CA	TRP	A	335	32.467	84.074	-1.718	1.00 15.96
ATOM	506	C	TRP	A	335	33.009	83.334	-2.963	1.00 18.59
ATOM	507	O	TRP	A	335	32.468	82.297	-3.360	1.00 20.05
ATOM	508	CB	TRP	A	335	31.554	85.252	-2.108	1.00 15.63
ATOM	509	CG	TRP	A	335	32.165	86.212	-3.056	1.00 13.54
ATOM	510	CD1	TRP	A	335	32.908	87.306	-2.753	1.00 11.75
ATOM	511	CD2	TRP	A	335	32.175	86.098	-4.486	1.00 15.51
ATOM	512	NE1	TRP	A	335	33.389	87.876	-3.900	1.00 13.51
ATOM	513	CE2	TRP	A	335	32.953	87.147	-4.983	1.00 16.55
ATOM	514	CE3	TRP	A	335	31.592	85.196	-5.395	1.00 15.54
ATOM	515	CZ2	TRP	A	335	33.184	87.330	-6.357	1.00 16.36
ATOM	516	CZ3	TRP	A	335	31.817	85.376	-6.758	1.00 13.43
ATOM	517	CH2	TRP	A	335	32.604	86.433	-7.222	1.00 15.29
ATOM	518	N	MET	A	336	34.084	83.850	-3.564	1.00 19.76
ATOM	519	CA	MET	A	336	34.680	83.226	-4.746	1.00 18.53
ATOM	520	C	MET	A	336	35.102	81.806	-4.427	1.00 16.57
ATOM	521	O	MET	A	336	34.711	80.840	-5.084	1.00 13.78
ATOM	522	CB	MET	A	336	35.898	84.018	-5.183	1.00 25.38
ATOM	523	CG	MET	A	336	36.622	83.455	-6.405	1.00 32.05
ATOM	524	SD	MET	A	336	35.649	83.602	-7.882	1.00 40.49
ATOM	525	CE	MET	A	336	36.142	85.307	-8.404	1.00 37.86
ATOM	526	N	GLU	A	337	35.915	81.695	-3.390	1.00 14.84
ATOM	527	CA	GLU	A	337	36.403	80.413	-2.964	1.00 12.50
ATOM	528	C	GLU	A	337	35.278	79.455	-2.578	1.00 12.56
ATOM	529	O	GLU	A	337	35.328	78.295	-2.922	1.00 13.22
ATOM	530	CB	GLU	A	337	37.372	80.604	-1.810	1.00 8.55
ATOM	531	CG	GLU	A	337	38.383	79.505	-1.706	1.00 14.40
ATOM	532	CD	GLU	A	337	39.372	79.719	-0.553	1.00 18.30
ATOM	533	OE1	GLU	A	337	39.685	80.890	-0.242	1.00 18.01
ATOM	534	OE2	GLU	A	337	39.845	78.720	0.038	1.00 15.07
ATOM	535	N	VAL	A	338	34.256	79.935	-1.877	1.00 12.46
ATOM	536	CA	VAL	A	338	33.161	79.069	-1.464	1.00 11.85
ATOM	537	C	VAL	A	338	32.382	78.626	-2.699	1.00 13.28
ATOM	538	O	VAL	A	338	31.961	77.470	-2.799	1.00 10.19
ATOM	539	CB	VAL	A	338	32.254	79.802	-0.408	1.00 15.77

ATOM	540	CG1	VAL	A	338	30.938	79.099	-0.206	1.00	16.03
ATOM	541	CG2	VAL	A	338	32.973	79.849	0.922	1.00	15.48
ATOM	542	N	LEU	A	339	32.211	79.522	-3.669	1.00	15.67
ATOM	543	CA	LEU	A	339	31.494	79.131	-4.876	1.00	17.55
ATOM	544	C	LEU	A	339	32.298	78.064	-5.590	1.00	18.67
ATOM	545	O	LEU	A	339	31.751	77.065	-6.047	1.00	18.92
ATOM	546	CB	LEU	A	339	31.275	80.324	-5.809	1.00	20.11
ATOM	547	CG	LEU	A	339	30.055	81.239	-5.647	1.00	19.03
ATOM	548	CD1	LEU	A	339	30.110	82.244	-6.767	1.00	19.53
ATOM	549	CD2	LEU	A	339	28.753	80.479	-5.709	1.00	17.35
ATOM	550	N	MET	A	340	33.607	78.276	-5.679	1.00	17.94
ATOM	551	CA	MET	A	340	34.473	77.305	-6.328	1.00	20.80
ATOM	552	C	MET	A	340	34.399	75.930	-5.664	1.00	22.16
ATOM	553	O	MET	A	340	34.195	74.927	-6.343	1.00	25.64
ATOM	554	CB	MET	A	340	35.907	77.825	-6.350	1.00	21.88
ATOM	555	CG	MET	A	340	36.054	79.100	-7.160	1.00	22.21
ATOM	556	SD	MET	A	340	37.744	79.436	-7.509	1.00	22.03
ATOM	557	CE	MET	A	340	37.603	80.420	-8.952	1.00	22.39
ATOM	558	N	MET	A	341	34.554	75.883	-4.345	1.00	21.23
ATOM	559	CA	MET	A	341	34.469	74.623	-3.609	1.00	22.72
ATOM	560	C	MET	A	341	33.159	73.900	-3.928	1.00	25.03
ATOM	561	O	MET	A	341	33.131	72.683	-4.124	1.00	26.27
ATOM	562	CB	MET	A	341	34.524	74.870	-2.104	1.00	20.25
ATOM	563	CG	MET	A	341	35.901	75.000	-1.516	1.00	20.06
ATOM	564	SD	MET	A	341	36.855	73.482	-1.656	1.00	27.93
ATOM	565	CE	MET	A	341	35.893	72.410	-0.741	1.00	20.39
ATOM	566	N	GLY	A	342	32.069	74.655	-3.974	1.00	26.08
ATOM	567	CA	GLY	A	342	30.776	74.061	-4.252	1.00	25.83
ATOM	568	C	GLY	A	342	30.671	73.519	-5.663	1.00	25.47
ATOM	569	O	GLY	A	342	30.003	72.519	-5.907	1.00	24.31
ATOM	586	N	TRP	A	345	32.604	70.110	-5.820	1.00	31.56
ATOM	587	CA	TRP	A	345	31.935	68.990	-5.176	1.00	31.51
ATOM	588	C	TRP	A	345	30.811	68.380	-6.031	1.00	34.86
ATOM	589	O	TRP	A	345	30.627	67.151	-6.056	1.00	34.73
ATOM	590	CB	TRP	A	345	31.419	69.408	-3.800	1.00	24.78
ATOM	591	CG	TRP	A	345	30.665	68.349	-3.123	1.00	21.06
ATOM	592	CD1	TRP	A	345	29.319	68.289	-2.975	1.00	21.80
ATOM	593	CD2	TRP	A	345	31.191	67.164	-2.503	1.00	22.45
ATOM	594	NE1	TRP	A	345	28.964	67.138	-2.297	1.00	23.41
ATOM	595	CE2	TRP	A	345	30.099	66.429	-1.997	1.00	22.74

ATOM	596	CE3	TRP	A	345	32.478	66.645	-2.328	1.00	23.11
ATOM	597	CZ2	TRP	A	345	30.254	65.205	-1.329	1.00	21.55
ATOM	598	CZ3	TRP	A	345	32.629	65.422	-1.663	1.00	22.09
ATOM	599	CH2	TRP	A	345	31.520	64.722	-1.175	1.00	21.02
ATOM	600	N	ARG	A	346	30.075	69.235	-6.741	1.00	36.80
ATOM	601	CA	ARG	A	346	28.987	68.780	-7.601	1.00	37.33
ATOM	602	C	ARG	A	346	29.578	68.037	-8.797	1.00	39.47
ATOM	603	O	ARG	A	346	29.037	67.033	-9.270	1.00	39.87
ATOM	604	CB	ARG	A	346	28.168	69.979	-8.100	1.00	35.61
ATOM	605	CG	ARG	A	346	27.515	70.790	-6.996	1.00	35.27
ATOM	606	CD	ARG	A	346	26.483	71.733	-7.560	1.00	32.82
ATOM	607	NE	ARG	A	346	27.065	72.830	-8.323	1.00	29.79
ATOM	608	CZ	ARG	A	346	27.472	73.975	-7.788	1.00	27.93
ATOM	609	NH1	ARG	A	346	27.362	74.176	-6.487	1.00	26.25
ATOM	610	NH2	ARG	A	346	27.974	74.924	-8.558	1.00	27.25
ATOM	625	N	ASP	A	349	32.433	63.755	-9.263	1.00	48.72
ATOM	626	CA	ASP	A	349	32.284	62.462	-9.916	1.00	49.63
ATOM	627	C	ASP	A	349	32.051	62.517	-11.430	1.00	50.48
ATOM	628	O	ASP	A	349	31.770	61.496	-12.047	1.00	52.40
ATOM	629	CB	ASP	A	349	31.145	61.681	-9.247	1.00	50.96
ATOM	630	CG	ASP	A	349	31.397	61.433	-7.762	1.00	54.14
ATOM	631	OD1	ASP	A	349	32.563	61.178	-7.397	1.00	57.25
ATOM	632	OD2	ASP	A	349	30.437	61.476	-6.960	1.00	54.83
ATOM	695	N	PRO	A	358	22.357	71.048	-12.407	1.00	51.18
ATOM	696	CA	PRO	A	358	21.930	69.832	-13.105	1.00	52.77
ATOM	697	C	PRO	A	358	21.782	70.051	-14.600	1.00	54.38
ATOM	698	O	PRO	A	358	22.245	69.241	-15.402	1.00	56.29
ATOM	699	CB	PRO	A	358	20.612	69.487	-12.420	1.00	51.61
ATOM	700	CG	PRO	A	358	20.875	69.898	-11.008	1.00	51.81
ATOM	701	CD	PRO	A	358	21.546	71.259	-11.195	1.00	52.76
ATOM	996	N	TYR	A	397	34.120	67.559	3.349	1.00	24.82
ATOM	997	CA	TYR	A	397	33.800	68.689	2.487	1.00	23.38
ATOM	998	C	TYR	A	397	33.126	69.782	3.289	1.00	22.45
ATOM	999	O	TYR	A	397	33.530	70.937	3.245	1.00	23.10
ATOM	1000	CB	TYR	A	397	32.879	68.208	1.359	1.00	25.09
ATOM	1001	CG	TYR	A	397	32.138	69.291	0.571	1.00	25.87
ATOM	1002	CD1	TYR	A	397	32.822	70.219	-0.213	1.00	24.58
ATOM	1003	CD2	TYR	A	397	30.744	69.374	0.609	1.00	24.99
ATOM	1004	CE1	TYR	A	397	32.136	71.204	-0.939	1.00	24.05
ATOM	1005	CE2	TYR	A	397	30.050	70.349	-0.109	1.00	24.00

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ATOM   1006  CZ  TYR A 397      30.746  71.261  -0.878  1.00 26.24
ATOM   1007  OH  TYR A 397      30.034  72.230  -1.569  1.00 29.36
ATOM   1008  N   LEU A 398      32.110  69.411   4.049  1.00 22.21
ATOM   1009  CA  LEU A 398      31.397  70.397   4.835  1.00 22.58
ATOM   1010  C   LEU A 398      32.272  71.129   5.849  1.00 22.08
ATOM   1011  O   LEU A 398      32.127  72.339   6.027  1.00 22.04
ATOM   1012  CB  LEU A 398      30.195  69.757   5.539  1.00 23.08
ATOM   1013  CG  LEU A 398      29.100  69.090   4.679  1.00 24.43
ATOM   1014  CD1 LEU A 398      27.860  68.904   5.536  1.00 23.58
ATOM   1015  CD2 LEU A 398      28.740  69.931   3.465  1.00 23.50
ATOM   1029  N   LYS A 401      34.605  73.520   4.066  1.00 17.69
ATOM   1030  CA  LYS A 401      33.897  74.681   3.542  1.00 17.79
ATOM   1031  C   LYS A 401      33.763  75.765   4.575  1.00 17.99
ATOM   1032  O   LYS A 401      34.004  76.930   4.301  1.00 19.98
ATOM   1033  CB  LYS A 401      32.510  74.284   3.068  1.00 19.62
ATOM   1034  CG  LYS A 401      31.907  75.273   2.112  1.00 22.29
ATOM   1035  CD  LYS A 401      30.912  74.581   1.156  1.00 24.70
ATOM   1036  CE  LYS A 401      29.552  74.361   1.798  1.00 24.63
ATOM   1037  NZ  LYS A 401      28.970  75.682   2.242  1.00 28.13
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GR Homology Model Site II Residues (ref. GR_icm_aligned.pdb)

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ATOM    103  N   GLU A 537     -11.080   4.969 -10.004  1.00 20.00
ATOM    104  CA  GLU A 537     -10.913   3.599 -10.490  1.00 20.00
ATOM    105  C   GLU A 537     -10.384   3.551 -11.927  1.00 20.00
ATOM    106  O   GLU A 537      -9.790   2.536 -12.306  1.00 20.00
ATOM    107  CB  GLU A 537     -12.267   2.897 -10.362  1.00 20.00
ATOM    108  CG  GLU A 537     -12.225   1.397 -10.662  1.00 20.00
ATOM    109  CD  GLU A 537     -12.502   1.114 -12.138  1.00 20.00
ATOM    110  OE1 GLU A 537     -12.954   2.042 -12.797  1.00 20.00
ATOM    111  OE2 GLU A 537     -12.518  -0.057 -12.489  1.00 20.00
ATOM    112  N   VAL A 538     -10.481   4.647 -12.662  1.00 20.00
ATOM    113  CA  VAL A 538      -9.938   4.688 -14.022  1.00 20.00
ATOM    114  C   VAL A 538      -8.508   5.243 -14.060  1.00 20.00
ATOM    115  O   VAL A 538      -7.739   4.908 -14.969  1.00 20.00
ATOM    116  CB  VAL A 538     -10.880   5.542 -14.872  1.00 20.00
ATOM    117  CG1 VAL A 538     -10.316   5.838 -16.259  1.00 20.00
ATOM    118  CG2 VAL A 538     -12.249   4.880 -14.995  1.00 20.00
ATOM    119  N   ILE A 539      -8.123   5.996 -13.041  1.00 20.00
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ATOM	120	CA	ILE	A	539	-6.742	6.497	-12.978	1.00	20.00
ATOM	121	C	ILE	A	539	-5.858	5.612	-12.099	1.00	20.00
ATOM	122	O	ILE	A	539	-4.647	5.839	-11.983	1.00	20.00
ATOM	123	CB	ILE	A	539	-6.734	7.967	-12.548	1.00	20.00
ATOM	124	CG1	ILE	A	539	-7.332	8.228	-11.167	1.00	20.00
ATOM	125	CG2	ILE	A	539	-7.441	8.818	-13.596	1.00	20.00
ATOM	126	CD1	ILE	A	539	-6.287	8.243	-10.060	1.00	20.00
ATOM	127	N	GLU	A	540	-6.479	4.616	-11.488	1.00	20.00
ATOM	128	CA	GLU	A	540	-5.766	3.576	-10.744	1.00	20.00
ATOM	129	C	GLU	A	540	-4.822	2.810	-11.678	1.00	20.00
ATOM	130	O	GLU	A	540	-5.227	2.388	-12.765	1.00	20.00
ATOM	131	CB	GLU	A	540	-6.843	2.636	-10.200	1.00	20.00
ATOM	132	CG	GLU	A	540	-6.313	1.647	-9.170	1.00	20.00
ATOM	133	CD	GLU	A	540	-5.839	2.402	-7.932	1.00	20.00
ATOM	134	OE1	GLU	A	540	-6.459	3.406	-7.607	1.00	20.00
ATOM	135	OE2	GLU	A	540	-4.842	1.988	-7.358	1.00	20.00
ATOM	136	N	PRO	A	541	-3.571	2.672	-11.264	1.00	20.00
ATOM	137	CA	PRO	A	541	-2.549	1.983	-12.062	1.00	20.00
ATOM	138	C	PRO	A	541	-2.768	0.470	-12.159	1.00	20.00
ATOM	139	O	PRO	A	541	-3.893	-0.042	-12.120	1.00	20.00
ATOM	140	CB	PRO	A	541	-1.247	2.285	-11.386	1.00	20.00
ATOM	141	CG	PRO	A	541	-1.524	3.000	-10.074	1.00	20.00
ATOM	142	CD	PRO	A	541	-3.028	3.202	-10.012	1.00	20.00
ATOM	143	N	GLU	A	542	-1.656	-0.223	-12.330	1.00	20.00
ATOM	144	CA	GLU	A	542	-1.675	-1.669	-12.569	1.00	20.00
ATOM	145	C	GLU	A	542	-1.033	-2.428	-11.404	1.00	20.00
ATOM	146	O	GLU	A	542	-0.112	-1.909	-10.762	1.00	20.00
ATOM	147	CB	GLU	A	542	-0.893	-1.901	-13.868	1.00	20.00
ATOM	148	CG	GLU	A	542	-0.941	-3.337	-14.389	1.00	20.00
ATOM	149	CD	GLU	A	542	-2.382	-3.754	-14.681	1.00	20.00
ATOM	150	OE1	GLU	A	542	-2.844	-3.471	-15.775	1.00	20.00
ATOM	151	OE2	GLU	A	542	-3.015	-4.268	-13.766	1.00	20.00
ATOM	152	N	VAL	A	543	-1.564	-3.605	-11.102	1.00	20.00
ATOM	153	CA	VAL	A	543	-0.902	-4.511	-10.154	1.00	20.00
ATOM	154	C	VAL	A	543	0.442	-4.922	-10.758	1.00	20.00
ATOM	155	O	VAL	A	543	0.543	-5.236	-11.950	1.00	20.00
ATOM	156	CB	VAL	A	543	-1.806	-5.720	-9.890	1.00	20.00
ATOM	157	CG1	VAL	A	543	-2.193	-6.445	-11.175	1.00	20.00
ATOM	158	CG2	VAL	A	543	-1.191	-6.692	-8.887	1.00	20.00
ATOM	334	N	LEU	A	566	10.458	-4.244	-6.551	1.00	20.00

ATOM	335	CA	LEU	A	566	9.019	-3.973	-6.485	1.00 20.00
ATOM	336	C	LEU	A	566	8.726	-2.637	-5.801	1.00 20.00
ATOM	337	O	LEU	A	566	7.849	-1.905	-6.272	1.00 20.00
ATOM	338	CB	LEU	A	566	8.363	-5.104	-5.708	1.00 20.00
ATOM	339	CG	LEU	A	566	6.853	-4.933	-5.626	1.00 20.00
ATOM	340	CD1	LEU	A	566	6.214	-4.892	-7.011	1.00 20.00
ATOM	341	CD2	LEU	A	566	6.244	-6.046	-4.787	1.00 20.00
ATOM	361	N	GLN	A	570	6.584	0.298	-7.548	1.00 20.00
ATOM	362	CA	GLN	A	570	5.437	0.936	-6.899	1.00 20.00
ATOM	363	C	GLN	A	570	5.643	2.432	-6.693	1.00 20.00
ATOM	364	O	GLN	A	570	4.656	3.173	-6.717	1.00 20.00
ATOM	365	CB	GLN	A	570	5.191	0.262	-5.558	1.00 20.00
ATOM	366	CG	GLN	A	570	4.794	-1.197	-5.748	1.00 20.00
ATOM	367	CD	GLN	A	570	4.596	-1.865	-4.394	1.00 20.00
ATOM	368	OE1	GLN	A	570	5.477	-2.575	-3.898	1.00 20.00
ATOM	369	NE2	GLN	A	570	3.451	-1.593	-3.792	1.00 20.00
ATOM	370	N	VAL	A	571	6.883	2.894	-6.730	1.00 20.00
ATOM	371	CA	VAL	A	571	7.140	4.333	-6.668	1.00 20.00
ATOM	372	C	VAL	A	571	6.890	4.996	-8.018	1.00 20.00
ATOM	373	O	VAL	A	571	6.212	6.032	-8.062	1.00 20.00
ATOM	374	CB	VAL	A	571	8.587	4.568	-6.242	1.00 20.00
ATOM	375	CG1	VAL	A	571	8.981	6.032	-6.395	1.00 20.00
ATOM	376	CG2	VAL	A	571	8.828	4.097	-4.813	1.00 20.00
ATOM	377	N	ILE	A	572	7.169	4.290	-9.103	1.00 20.00
ATOM	378	CA	ILE	A	572	6.914	4.887	-10.416	1.00 20.00
ATOM	379	C	ILE	A	572	5.436	4.736	-10.799	1.00 20.00
ATOM	380	O	ILE	A	572	4.871	5.667	-11.388	1.00 20.00
ATOM	381	CB	ILE	A	572	7.910	4.311	-11.440	1.00 20.00
ATOM	382	CG1	ILE	A	572	7.921	5.073	-12.768	1.00 20.00
ATOM	383	CG2	ILE	A	572	7.686	2.827	-11.702	1.00 20.00
ATOM	384	CD1	ILE	A	572	6.842	4.607	-13.742	1.00 20.00
ATOM	385	N	ALA	A	573	4.754	3.770	-10.201	1.00 20.00
ATOM	386	CA	ALA	A	573	3.309	3.672	-10.400	1.00 20.00
ATOM	387	C	ALA	A	573	2.561	4.657	-9.507	1.00 20.00
ATOM	388	O	ALA	A	573	1.566	5.243	-9.950	1.00 20.00
ATOM	389	CB	ALA	A	573	2.858	2.251	-10.080	1.00 20.00
ATOM	390	N	ALA	A	574	3.173	5.031	-8.394	1.00 20.00
ATOM	391	CA	ALA	A	574	2.562	6.013	-7.500	1.00 20.00
ATOM	392	C	ALA	A	574	2.777	7.440	-7.981	1.00 20.00
ATOM	393	O	ALA	A	574	1.870	8.260	-7.816	1.00 20.00

ATOM	394	CB	ALA	A	574	3.146	5.858	-6.101	1.00 20.00
ATOM	395	N	VAL	A	575	3.827	7.690	-8.749	1.00 20.00
ATOM	396	CA	VAL	A	575	3.972	9.034	-9.313	1.00 20.00
ATOM	397	C	VAL	A	575	3.152	9.174	-10.597	1.00 20.00
ATOM	398	O	VAL	A	575	2.598	10.253	-10.841	1.00 20.00
ATOM	399	CB	VAL	A	575	5.448	9.381	-9.531	1.00 20.00
ATOM	400	CG1	VAL	A	575	6.158	8.438	-10.494	1.00 20.00
ATOM	401	CG2	VAL	A	575	5.612	10.825	-9.995	1.00 20.00
ATOM	402	N	LYS	A	576	2.810	8.050	-11.212	1.00 20.00
ATOM	403	CA	LYS	A	576	1.910	8.090	-12.364	1.00 20.00
ATOM	404	C	LYS	A	576	0.463	8.241	-11.898	1.00 20.00
ATOM	405	O	LYS	A	576	-0.273	9.074	-12.440	1.00 20.00
ATOM	406	CB	LYS	A	576	2.074	6.795	-13.151	1.00 20.00
ATOM	407	CG	LYS	A	576	1.273	6.824	-14.447	1.00 20.00
ATOM	408	CD	LYS	A	576	1.761	7.935	-15.372	1.00 20.00
ATOM	409	CE	LYS	A	576	3.218	7.728	-15.772	1.00 20.00
ATOM	410	NZ	LYS	A	576	3.687	8.826	-16.634	1.00 20.00
ATOM	411	N	TRP	A	577	0.174	7.673	-10.739	1.00 20.00
ATOM	412	CA	TRP	A	577	-1.144	7.819	-10.115	1.00 20.00
ATOM	413	C	TRP	A	577	-1.321	9.205	-9.494	1.00 20.00
ATOM	414	O	TRP	A	577	-2.398	9.800	-9.622	1.00 20.00
ATOM	415	CB	TRP	A	577	-1.242	6.744	-9.037	1.00 20.00
ATOM	416	CG	TRP	A	577	-2.481	6.797	-8.167	1.00 20.00
ATOM	417	CD1	TRP	A	577	-3.729	6.312	-8.478	1.00 20.00
ATOM	418	CD2	TRP	A	577	-2.577	7.356	-6.839	1.00 20.00
ATOM	419	NE1	TRP	A	577	-4.558	6.554	-7.433	1.00 20.00
ATOM	420	CE2	TRP	A	577	-3.911	7.181	-6.434	1.00 20.00
ATOM	421	CE3	TRP	A	577	-1.662	7.973	-5.997	1.00 20.00
ATOM	422	CZ2	TRP	A	577	-4.318	7.645	-5.190	1.00 20.00
ATOM	423	CZ3	TRP	A	577	-2.078	8.424	-4.751	1.00 20.00
ATOM	424	CH2	TRP	A	577	-3.399	8.263	-4.350	1.00 20.00
ATOM	596	N	SER	A	599	4.149	9.996	1.965	1.00 20.00
ATOM	597	CA	SER	A	599	3.110	8.965	1.912	1.00 20.00
ATOM	598	C	SER	A	599	3.534	7.679	1.209	1.00 20.00
ATOM	599	O	SER	A	599	2.773	6.704	1.271	1.00 20.00
ATOM	600	CB	SER	A	599	1.914	9.536	1.164	1.00 20.00
ATOM	601	OG	SER	A	599	2.316	9.748	-0.183	1.00 20.00
ATOM	602	N	TRP	A	600	4.769	7.593	0.733	1.00 20.00
ATOM	603	CA	TRP	A	600	5.156	6.475	-0.146	1.00 20.00
ATOM	604	C	TRP	A	600	5.137	5.113	0.553	1.00 20.00

ATOM	605	O	TRP	A	600	4.590	4.167	-0.029	1.00 20.00
ATOM	606	CB	TRP	A	600	6.549	6.733	-0.739	1.00 20.00
ATOM	607	CG	TRP	A	600	7.745	6.447	0.160	1.00 20.00
ATOM	608	CD1	TRP	A	600	8.085	7.097	1.327	1.00 20.00
ATOM	609	CD2	TRP	A	600	8.745	5.424	-0.037	1.00 20.00
ATOM	610	NE1	TRP	A	600	9.207	6.530	1.830	1.00 20.00
ATOM	611	CE2	TRP	A	600	9.637	5.524	1.046	1.00 20.00
ATOM	612	CE3	TRP	A	600	8.942	4.460	-1.016	1.00 20.00
ATOM	613	CZ2	TRP	A	600	10.720	4.663	1.131	1.00 20.00
ATOM	614	CZ3	TRP	A	600	10.027	3.599	-0.921	1.00 20.00
ATOM	615	CH2	TRP	A	600	10.914	3.699	0.147	1.00 20.00
ATOM	616	N	MET	A	601	5.381	5.092	1.856	1.00 20.00
ATOM	617	CA	MET	A	601	5.436	3.817	2.562	1.00 20.00
ATOM	618	C	MET	A	601	4.049	3.290	2.895	1.00 20.00
ATOM	619	O	MET	A	601	3.823	2.080	2.785	1.00 20.00
ATOM	620	CB	MET	A	601	6.242	3.989	3.842	1.00 20.00
ATOM	621	CG	MET	A	601	7.468	3.084	3.825	1.00 20.00
ATOM	622	SD	MET	A	601	7.126	1.318	3.636	1.00 20.00
ATOM	623	CE	MET	A	601	8.822	0.695	3.653	1.00 20.00
ATOM	624	N	PHE	A	602	3.076	4.172	3.039	1.00 20.00
ATOM	625	CA	PHE	A	602	1.745	3.653	3.323	1.00 20.00
ATOM	626	C	PHE	A	602	0.933	3.520	2.040	1.00 20.00
ATOM	627	O	PHE	A	602	0.010	2.702	1.997	1.00 20.00
ATOM	628	CB	PHE	A	602	1.018	4.502	4.354	1.00 20.00
ATOM	629	CG	PHE	A	602	-0.170	3.743	4.939	1.00 20.00
ATOM	630	CD1	PHE	A	602	-0.131	2.353	4.994	1.00 20.00
ATOM	631	CD2	PHE	A	602	-1.273	4.424	5.431	1.00 20.00
ATOM	632	CE1	PHE	A	602	-1.212	1.645	5.499	1.00 20.00
ATOM	633	CE2	PHE	A	602	-2.354	3.714	5.938	1.00 20.00
ATOM	634	CZ	PHE	A	602	-2.327	2.326	5.962	1.00 20.00
ATOM	635	N	LEU	A	603	1.401	4.109	0.955	1.00 20.00
ATOM	636	CA	LEU	A	603	0.750	3.834	-0.325	1.00 20.00
ATOM	637	C	LEU	A	603	1.106	2.426	-0.787	1.00 20.00
ATOM	638	O	LEU	A	603	0.195	1.633	-1.070	1.00 20.00
ATOM	639	CB	LEU	A	603	1.191	4.854	-1.369	1.00 20.00
ATOM	640	CG	LEU	A	603	0.668	6.252	-1.062	1.00 20.00
ATOM	641	CD1	LEU	A	603	1.188	7.258	-2.083	1.00 20.00
ATOM	642	CD2	LEU	A	603	-0.856	6.278	-1.015	1.00 20.00
ATOM	643	N	MET	A	604	2.348	2.028	-0.558	1.00 20.00
ATOM	644	CA	MET	A	604	2.746	0.674	-0.947	1.00 20.00

ATOM	645	C	MET	A	604	2.317	-0.384	0.076	1.00	20.00
ATOM	646	O	MET	A	604	1.938	-1.486	-0.344	1.00	20.00
ATOM	647	CB	MET	A	604	4.255	0.637	-1.195	1.00	20.00
ATOM	648	CG	MET	A	604	5.089	1.042	0.014	1.00	20.00
ATOM	649	SD	MET	A	604	6.873	1.110	-0.258	1.00	20.00
ATOM	650	CE	MET	A	604	7.149	-0.608	-0.746	1.00	20.00
ATOM	651	N	ALA	A	605	2.106	0.011	1.323	1.00	20.00
ATOM	652	CA	ALA	A	605	1.640	-0.947	2.331	1.00	20.00
ATOM	653	C	ALA	A	605	0.122	-1.102	2.349	1.00	20.00
ATOM	654	O	ALA	A	605	-0.370	-2.197	2.644	1.00	20.00
ATOM	655	CB	ALA	A	605	2.123	-0.501	3.704	1.00	20.00
ATOM	656	N	PHE	A	606	-0.597	-0.112	1.845	1.00	20.00
ATOM	657	CA	PHE	A	606	-2.052	-0.234	1.754	1.00	20.00
ATOM	658	C	PHE	A	606	-2.409	-0.954	0.461	1.00	20.00
ATOM	659	O	PHE	A	606	-3.386	-1.715	0.419	1.00	20.00
ATOM	660	CB	PHE	A	606	-2.665	1.161	1.767	1.00	20.00
ATOM	661	CG	PHE	A	606	-4.092	1.228	2.298	1.00	20.00
ATOM	662	CD1	PHE	A	606	-4.513	0.331	3.272	1.00	20.00
ATOM	663	CD2	PHE	A	606	-4.968	2.195	1.821	1.00	20.00
ATOM	664	CE1	PHE	A	606	-5.808	0.403	3.768	1.00	20.00
ATOM	665	CE2	PHE	A	606	-6.262	2.268	2.319	1.00	20.00
ATOM	666	CZ	PHE	A	606	-6.683	1.371	3.292	1.00	20.00
ATOM	667	N	ALA	A	607	-1.494	-0.893	-0.496	1.00	20.00
ATOM	668	CA	ALA	A	607	-1.629	-1.694	-1.711	1.00	20.00
ATOM	669	C	ALA	A	607	-1.379	-3.161	-1.389	1.00	20.00
ATOM	670	O	ALA	A	607	-2.225	-3.998	-1.718	1.00	20.00
ATOM	671	CB	ALA	A	607	-0.616	-1.213	-2.745	1.00	20.00
ATOM	684	N	TRP	A	610	-4.529	-4.496	0.500	1.00	20.00
ATOM	685	CA	TRP	A	610	-5.667	-4.797	-0.368	1.00	20.00
ATOM	686	C	TRP	A	610	-5.403	-5.914	-1.376	1.00	20.00
ATOM	687	O	TRP	A	610	-6.325	-6.688	-1.660	1.00	20.00
ATOM	688	CB	TRP	A	610	-5.999	-3.528	-1.132	1.00	20.00
ATOM	689	CG	TRP	A	610	-7.315	-3.587	-1.870	1.00	20.00
ATOM	690	CD1	TRP	A	610	-7.512	-3.767	-3.222	1.00	20.00
ATOM	691	CD2	TRP	A	610	-8.622	-3.458	-1.278	1.00	20.00
ATOM	692	NE1	TRP	A	610	-8.847	-3.743	-3.466	1.00	20.00
ATOM	693	CE2	TRP	A	610	-9.547	-3.552	-2.330	1.00	20.00
ATOM	694	CE3	TRP	A	610	-9.059	-3.259	0.025	1.00	20.00
ATOM	695	CZ2	TRP	A	610	-10.900	-3.436	-2.068	1.00	20.00
ATOM	696	CZ3	TRP	A	610	-10.418	-3.148	0.279	1.00	20.00

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ATOM    697  CH2 TRP A 610     -11.335  -3.235  -0.762  1.00 20.00
ATOM    698  N   ARG A 611      -4.156  -6.131  -1.756  1.00 20.00
ATOM    699  CA  ARG A 611      -3.861  -7.238  -2.668  1.00 20.00
ATOM    700  C   ARG A 611      -3.829  -8.565  -1.923  1.00 20.00
ATOM    701  O   ARG A 611      -4.278  -9.580  -2.467  1.00 20.00
ATOM    702  CB  ARG A 611      -2.519  -7.006  -3.348  1.00 20.00
ATOM    703  CG  ARG A 611      -2.552  -5.803  -4.281  1.00 20.00
ATOM    704  CD  ARG A 611      -1.201  -5.612  -4.954  1.00 20.00
ATOM    705  NE  ARG A 611      -0.138  -5.503  -3.943  1.00 20.00
ATOM    706  CZ  ARG A 611       0.984  -4.805  -4.125  1.00 20.00
ATOM    707  NH1 ARG A 611       1.197  -4.175  -5.283  1.00 20.00
ATOM    708  NH2 ARG A 611       1.898  -4.748  -3.154  1.00 20.00
ATOM    727  N   ARG A 614      -7.642  -9.259  -1.472  1.00 20.00
ATOM    728  CA  ARG A 614      -8.243  -9.807  -2.687  1.00 20.00
ATOM    729  C   ARG A 614      -7.722 -11.191  -3.065  1.00 20.00
ATOM    730  O   ARG A 614      -8.480 -12.164  -2.979  1.00 20.00
ATOM    731  CB  ARG A 614      -7.982  -8.840  -3.834  1.00 20.00
ATOM    732  CG  ARG A 614      -8.818  -7.576  -3.688  1.00 20.00
ATOM    733  CD  ARG A 614     -10.305  -7.915  -3.709  1.00 20.00
ATOM    734  NE  ARG A 614     -11.140  -6.705  -3.660  1.00 20.00
ATOM    735  CZ  ARG A 614     -11.850  -6.273  -4.706  1.00 20.00
ATOM    736  NH1 ARG A 614     -11.803  -6.934  -5.865  1.00 20.00
ATOM    737  NH2 ARG A 614     -12.598  -5.173  -4.597  1.00 20.00
ATOM    738  N   GLN A 615      -6.423 -11.316  -3.284  1.00 20.00
ATOM    739  CA  GLN A 615      -5.898 -12.536  -3.912  1.00 20.00
ATOM    740  C   GLN A 615      -5.649 -13.696  -2.939  1.00 20.00
ATOM    741  O   GLN A 615      -5.544 -14.844  -3.387  1.00 20.00
ATOM    742  CB  GLN A 615      -4.608 -12.166  -4.650  1.00 20.00
ATOM    743  CG  GLN A 615      -4.148 -13.276  -5.595  1.00 20.00
ATOM    744  CD  GLN A 615      -2.882 -12.878  -6.352  1.00 20.00
ATOM    745  OE1 GLN A 615      -2.647 -11.698  -6.641  1.00 20.00
ATOM    746  NE2 GLN A 615      -2.103 -13.886  -6.702  1.00 20.00
ATOM    810  N   PRO A 625       1.353 -10.802  -8.117  1.00 20.00
ATOM    811  CA  PRO A 625       0.837 -12.115  -8.533  1.00 20.00
ATOM    812  C   PRO A 625       1.938 -13.187  -8.632  1.00 20.00
ATOM    813  O   PRO A 625       1.677 -14.360  -8.344  1.00 20.00
ATOM    814  CB  PRO A 625       0.196 -11.871  -9.866  1.00 20.00
ATOM    815  CG  PRO A 625       0.452 -10.433 -10.295  1.00 20.00
ATOM    816  CD  PRO A 625       1.237  -9.785  -9.168  1.00 20.00
ATOM   1129  N   TYR A 663     -11.805   2.057  -0.132  1.00 20.00
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ATOM   1130  CA  TYR A 663     -10.353   1.872  -0.181  1.00 20.00
ATOM   1131  C   TYR A 663      -9.660   2.895  -1.077  1.00 20.00
ATOM   1132  O   TYR A 663      -8.661   3.484  -0.649  1.00 20.00
ATOM   1133  CB  TYR A 663     -10.054   0.473  -0.710  1.00 20.00
ATOM   1134  CG  TYR A 663      -8.576   0.255  -1.027  1.00 20.00
ATOM   1135  CD1 TYR A 663      -7.664   0.076   0.005  1.00 20.00
ATOM   1136  CD2 TYR A 663      -8.143   0.241  -2.348  1.00 20.00
ATOM   1137  CE1 TYR A 663      -6.318  -0.101  -0.284  1.00 20.00
ATOM   1138  CE2 TYR A 663      -6.797   0.067  -2.638  1.00 20.00
ATOM   1139  CZ  TYR A 663      -5.887  -0.099  -1.603  1.00 20.00
ATOM   1140  OH  TYR A 663      -4.550  -0.263  -1.885  1.00 20.00
ATOM   1141  N   LEU A 664     -10.297   3.279  -2.170  1.00 20.00
ATOM   1142  CA  LEU A 664      -9.673   4.228  -3.097  1.00 20.00
ATOM   1143  C   LEU A 664      -9.708   5.650  -2.549  1.00 20.00
ATOM   1144  O   LEU A 664      -8.688   6.352  -2.613  1.00 20.00
ATOM   1145  CB  LEU A 664     -10.414   4.173  -4.432  1.00 20.00
ATOM   1146  CG  LEU A 664      -9.675   3.386  -5.519  1.00 20.00
ATOM   1147  CD1 LEU A 664      -9.285   1.975  -5.097  1.00 20.00
ATOM   1148  CD2 LEU A 664     -10.512   3.325  -6.788  1.00 20.00
ATOM   1163  N   LYS A 667      -7.067   5.761   0.246  1.00 20.00
ATOM   1164  CA  LYS A 667      -5.708   5.727  -0.288  1.00 20.00
ATOM   1165  C   LYS A 667      -5.292   7.076  -0.870  1.00 20.00
ATOM   1166  O   LYS A 667      -4.158   7.509  -0.631  1.00 20.00
ATOM   1167  CB  LYS A 667      -5.665   4.646  -1.358  1.00 20.00
ATOM   1168  CG  LYS A 667      -4.275   4.476  -1.961  1.00 20.00
ATOM   1169  CD  LYS A 667      -4.239   3.443  -3.090  1.00 20.00
ATOM   1170  CE  LYS A 667      -4.633   4.000  -4.463  1.00 20.00
ATOM   1171  NZ  LYS A 667      -6.057   4.359  -4.580  1.00 20.00
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MR Homology Model Site II Residues (ref. MR_homo.pdb)

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ATOM     88  N   GLU   13      50.931  27.871  20.999  1.00  0.00
ATOM     89  CA  GLU   13      50.817  29.290  20.819  1.00  0.00
ATOM     90  CB  GLU   13      52.092  29.933  20.251  1.00  0.00
ATOM     91  CG  GLU   13      52.003  31.458  20.153  1.00  0.00
ATOM     92  CD  GLU   13      53.314  31.973  19.577  1.00  0.00
ATOM     93  OE1 GLU   13      54.151  31.126  19.165  1.00  0.00
ATOM     94  OE2 GLU   13      53.496  33.219  19.541  1.00  0.00
ATOM     95  C   GLU   13      49.713  29.586  19.852  1.00  0.00
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ATOM	96	O	GLU	13	48.968	30.550	20.026	1.00	0.00
ATOM	97	N	ASN	14	49.577	28.760	18.799	1.00	0.00
ATOM	98	CA	ASN	14	48.615	29.036	17.770	1.00	0.00
ATOM	99	CB	ASN	14	48.697	28.039	16.602	1.00	0.00
ATOM	100	CG	ASN	14	47.913	28.622	15.435	1.00	0.00
ATOM	101	OD1	ASN	14	47.172	29.591	15.587	1.00	0.00
ATOM	102	ND2	ASN	14	48.079	28.011	14.231	1.00	0.00
ATOM	103	C	ASN	14	47.213	28.992	18.312	1.00	0.00
ATOM	104	O	ASN	14	46.392	29.849	17.996	1.00	0.00
ATOM	105	N	ILE	15	46.916	27.976	19.141	1.00	0.00
ATOM	106	CA	ILE	15	45.633	27.682	19.725	1.00	0.00
ATOM	107	CB	ILE	15	45.577	26.305	20.331	1.00	0.00
ATOM	108	CG2	ILE	15	45.787	25.295	19.190	1.00	0.00
ATOM	109	CG1	ILE	15	46.580	26.147	21.485	1.00	0.00
ATOM	110	CD1	ILE	15	46.397	24.849	22.273	1.00	0.00
ATOM	111	C	ILE	15	45.189	28.695	20.741	1.00	0.00
ATOM	112	O	ILE	15	43.985	28.817	20.968	1.00	0.00
ATOM	113	N	GLU	16	46.132	29.383	21.429	1.00	0.00
ATOM	114	CA	GLU	16	45.791	30.312	22.480	1.00	0.00
ATOM	115	CB	GLU	16	46.950	31.203	22.966	1.00	0.00
ATOM	116	CG	GLU	16	47.969	30.501	23.864	1.00	0.00
ATOM	117	CD	GLU	16	47.425	30.438	25.288	1.00	0.00
ATOM	118	OE1	GLU	16	47.568	31.446	26.032	1.00	0.00
ATOM	119	OE2	GLU	16	46.859	29.373	25.652	1.00	0.00
ATOM	120	C	GLU	16	44.714	31.238	22.012	1.00	0.00
ATOM	121	O	GLU	16	44.677	31.697	20.871	1.00	0.00
ATOM	122	N	PRO	17	43.806	31.494	22.913	1.00	0.00
ATOM	123	CA	PRO	17	42.694	32.337	22.590	1.00	0.00
ATOM	124	CD	PRO	17	43.472	30.530	23.945	1.00	0.00
ATOM	125	CB	PRO	17	41.611	32.034	23.608	1.00	0.00
ATOM	126	CG	PRO	17	42.309	31.194	24.693	1.00	0.00
ATOM	127	C	PRO	17	43.075	33.773	22.516	1.00	0.00
ATOM	128	O	PRO	17	44.063	34.167	23.133	1.00	0.00
ATOM	129	N	GLU	18	42.299	34.566	21.753	1.00	0.00
ATOM	130	CA	GLU	18	42.588	35.960	21.624	1.00	0.00
ATOM	131	CB	GLU	18	42.033	36.612	20.340	1.00	0.00
ATOM	132	CG	GLU	18	40.509	36.606	20.224	1.00	0.00
ATOM	133	CD	GLU	18	40.113	37.261	18.904	1.00	0.00
ATOM	134	OE1	GLU	18	40.910	38.078	18.369	1.00	0.00
ATOM	135	OE2	GLU	18	38.998	36.945	18.411	1.00	0.00

ATOM	136	C	GLU	18	42.029	36.646	22.830	1.00	0.00
ATOM	137	O	GLU	18	41.272	36.057	23.599	1.00	0.00
ATOM	138	N	ILE	19	42.420	37.916	23.039	1.00	0.00
ATOM	139	CA	ILE	19	41.997	38.627	24.209	1.00	0.00
ATOM	140	CB	ILE	19	42.419	40.062	24.273	1.00	0.00
ATOM	141	CG2	ILE	19	41.512	40.845	23.311	1.00	0.00
ATOM	142	CG1	ILE	19	42.331	40.567	25.722	1.00	0.00
ATOM	143	CD1	ILE	19	43.339	39.889	26.650	1.00	0.00
ATOM	144	C	ILE	19	40.510	38.630	24.271	1.00	0.00
ATOM	145	O	ILE	19	39.822	38.676	23.253	1.00	0.00
ATOM	315	N	LEU	42	33.148	37.906	32.521	1.00	0.00
ATOM	316	CA	LEU	42	34.407	37.687	31.875	1.00	0.00
ATOM	317	CB	LEU	42	35.532	38.502	32.546	1.00	0.00
ATOM	318	CG	LEU	42	36.931	38.342	31.921	1.00	0.00
ATOM	319	CD2	LEU	42	38.021	38.928	32.836	1.00	0.00
ATOM	320	CD1	LEU	42	36.974	38.932	30.502	1.00	0.00
ATOM	321	C	LEU	42	34.735	36.234	32.024	1.00	0.00
ATOM	322	O	LEU	42	35.168	35.574	31.081	1.00	0.00
ATOM	323	N	ALA	43	34.488	35.691	33.229	1.00	0.00
ATOM	324	CA	ALA	43	34.795	34.322	33.518	1.00	0.00
ATOM	325	CB	ALA	43	34.435	33.917	34.957	1.00	0.00
ATOM	326	C	ALA	43	34.012	33.442	32.593	1.00	0.00
ATOM	327	O	ALA	43	34.530	32.444	32.096	1.00	0.00
ATOM	341	N	GLN	46	35.564	33.506	29.250	1.00	0.00
ATOM	342	CA	GLN	46	36.820	32.822	29.264	1.00	0.00
ATOM	343	CB	GLN	46	37.738	33.286	30.411	1.00	0.00
ATOM	344	CG	GLN	46	38.134	34.757	30.230	1.00	0.00
ATOM	345	CD	GLN	46	39.055	35.221	31.353	1.00	0.00
ATOM	346	OE1	GLN	46	38.899	34.870	32.521	1.00	0.00
ATOM	347	NE2	GLN	46	40.057	36.060	30.978	1.00	0.00
ATOM	348	C	GLN	46	36.587	31.343	29.341	1.00	0.00
ATOM	349	O	GLN	46	37.340	30.564	28.760	1.00	0.00
ATOM	350	N	MET	47	35.544	30.909	30.075	1.00	0.00
ATOM	351	CA	MET	47	35.276	29.502	30.196	1.00	0.00
ATOM	352	CB	MET	47	34.190	29.155	31.227	1.00	0.00
ATOM	353	CG	MET	47	34.688	29.305	32.667	1.00	0.00
ATOM	354	SD	MET	47	33.526	28.732	33.942	1.00	0.00
ATOM	355	CE	MET	47	32.462	30.200	33.859	1.00	0.00
ATOM	356	C	MET	47	34.895	28.928	28.863	1.00	0.00
ATOM	357	O	MET	47	35.288	27.809	28.537	1.00	0.00

ATOM	358	N	ILE	48	34.124	29.669	28.045	1.00	0.00
ATOM	359	CA	ILE	48	33.739	29.134	26.768	1.00	0.00
ATOM	360	CB	ILE	48	32.787	30.022	25.996	1.00	0.00
ATOM	361	CG2	ILE	48	33.553	31.222	25.419	1.00	0.00
ATOM	362	CG1	ILE	48	32.045	29.216	24.915	1.00	0.00
ATOM	363	CD1	ILE	48	32.950	28.621	23.839	1.00	0.00
ATOM	364	C	ILE	48	35.001	28.931	25.985	1.00	0.00
ATOM	365	O	ILE	48	35.171	27.932	25.288	1.00	0.00
ATOM	366	N	GLN	49	35.934	29.887	26.124	1.00	0.00
ATOM	367	CA	GLN	49	37.205	29.941	25.465	1.00	0.00
ATOM	368	CB	GLN	49	37.951	31.181	25.969	1.00	0.00
ATOM	369	CG	GLN	49	39.382	31.319	25.491	1.00	0.00
ATOM	370	CD	GLN	49	39.948	32.566	26.158	1.00	0.00
ATOM	371	OE1	GLN	49	40.213	33.581	25.516	1.00	0.00
ATOM	372	NE2	GLN	49	40.130	32.488	27.504	1.00	0.00
ATOM	373	C	GLN	49	38.023	28.742	25.840	1.00	0.00
ATOM	374	O	GLN	49	38.668	28.133	24.987	1.00	0.00
ATOM	375	N	VAL	50	38.021	28.376	27.136	1.00	0.00
ATOM	376	CA	VAL	50	38.816	27.273	27.593	1.00	0.00
ATOM	377	CB	VAL	50	38.842	27.108	29.089	1.00	0.00
ATOM	378	CG1	VAL	50	37.495	26.564	29.581	1.00	0.00
ATOM	379	CG2	VAL	50	40.035	26.208	29.442	1.00	0.00
ATOM	380	C	VAL	50	38.308	26.008	26.980	1.00	0.00
ATOM	381	O	VAL	50	39.088	25.128	26.622	1.00	0.00
ATOM	382	N	VAL	51	36.976	25.875	26.849	1.00	0.00
ATOM	383	CA	VAL	51	36.414	24.678	26.294	1.00	0.00
ATOM	384	CB	VAL	51	34.912	24.692	26.305	1.00	0.00
ATOM	385	CG1	VAL	51	34.404	23.377	25.692	1.00	0.00
ATOM	386	CG2	VAL	51	34.430	24.941	27.746	1.00	0.00
ATOM	387	C	VAL	51	36.876	24.541	24.873	1.00	0.00
ATOM	388	O	VAL	51	37.293	23.464	24.449	1.00	0.00
ATOM	389	N	LYS	52	36.835	25.647	24.103	1.00	0.00
ATOM	390	CA	LYS	52	37.212	25.627	22.715	1.00	0.00
ATOM	391	CB	LYS	52	37.071	27.003	22.044	1.00	0.00
ATOM	392	CG	LYS	52	35.621	27.463	21.919	1.00	0.00
ATOM	393	CD	LYS	52	34.766	26.499	21.096	1.00	0.00
ATOM	394	CE	LYS	52	33.303	26.924	20.964	1.00	0.00
ATOM	395	NZ	LYS	52	32.566	25.933	20.150	1.00	0.00
ATOM	396	C	LYS	52	38.653	25.243	22.614	1.00	0.00
ATOM	397	O	LYS	52	39.040	24.430	21.776	1.00	0.00

	ATOM	398	N	TRP	53	39.475	25.822	23.501	1.00	0.00
	ATOM	399	CA	TRP	53	40.895	25.630	23.554	1.00	0.00
	ATOM	400	CB	TRP	53	41.475	26.501	24.686	1.00	0.00
	ATOM	401	CG	TRP	53	42.945	26.376	25.000	1.00	0.00
5	ATOM	402	CD2	TRP	53	43.439	25.944	26.277	1.00	0.00
	ATOM	403	CD1	TRP	53	44.038	26.694	24.249	1.00	0.00
	ATOM	404	NE1	TRP	53	45.184	26.480	24.978	1.00	0.00
	ATOM	405	CE2	TRP	53	44.830	26.022	26.229	1.00	0.00
	ATOM	406	CE3	TRP	53	42.784	25.529	27.401	1.00	0.00
10	ATOM	407	CZ2	TRP	53	45.593	25.682	27.310	1.00	0.00
	ATOM	408	CZ3	TRP	53	43.556	25.176	28.485	1.00	0.00
	ATOM	409	CH2	TRP	53	44.934	25.251	28.440	1.00	0.00
	ATOM	410	C	TRP	53	41.189	24.182	23.822	1.00	0.00
	ATOM	411	O	TRP	53	42.059	23.580	23.197	1.00	0.00
15	ATOM	581	N	SER	75	39.887	22.457	37.038	1.00	0.00
	ATOM	582	CA	SER	75	40.947	23.398	36.753	1.00	0.00
	ATOM	583	CB	SER	75	41.896	22.887	35.651	1.00	0.00
	ATOM	584	OG	SER	75	41.214	22.807	34.408	1.00	0.00
	ATOM	585	C	SER	75	40.579	24.808	36.360	1.00	0.00
20	ATOM	586	O	SER	75	41.475	25.646	36.275	1.00	0.00
	ATOM	587	N	TRP	76	39.302	25.147	36.119	1.00	0.00
	ATOM	588	CA	TRP	76	39.003	26.424	35.509	1.00	0.00
	ATOM	589	CB	TRP	76	37.491	26.643	35.310	1.00	0.00
	ATOM	590	CG	TRP	76	36.673	26.648	36.581	1.00	0.00
25	ATOM	591	CD2	TRP	76	36.356	27.830	37.333	1.00	0.00
	ATOM	592	CD1	TRP	76	36.081	25.605	37.232	1.00	0.00
	ATOM	593	NE1	TRP	76	35.419	26.063	38.347	1.00	0.00
	ATOM	594	CE2	TRP	76	35.579	27.431	38.420	1.00	0.00
	ATOM	595	CE3	TRP	76	36.683	29.140	37.132	1.00	0.00
30	ATOM	596	CZ2	TRP	76	35.116	28.340	39.328	1.00	0.00
	ATOM	597	CZ3	TRP	76	36.216	30.055	38.051	1.00	0.00
	ATOM	598	CH2	TRP	76	35.448	29.662	39.127	1.00	0.00
	ATOM	599	C	TRP	76	39.550	27.596	36.285	1.00	0.00
	ATOM	600	O	TRP	76	40.098	28.524	35.690	1.00	0.00
35	ATOM	601	N	MET	77	39.427	27.603	37.623	1.00	0.00
	ATOM	602	CA	MET	77	39.884	28.723	38.406	1.00	0.00
	ATOM	603	CB	MET	77	39.653	28.497	39.912	1.00	0.00
	ATOM	604	CG	MET	77	39.840	29.734	40.795	1.00	0.00
	ATOM	605	SD	MET	77	38.411	30.858	40.857	1.00	0.00
40	ATOM	606	CE	MET	77	38.558	31.470	39.157	1.00	0.00

ATOM	607	C	MET	77	41.366	28.887	38.235	1.00	0.00
ATOM	608	O	MET	77	41.867	30.002	38.088	1.00	0.00
ATOM	609	N	CYS	78	42.110	27.767	38.260	1.00	0.00
ATOM	610	CA	CYS	78	43.542	27.811	38.167	1.00	0.00
ATOM	611	CB	CYS	78	44.185	26.422	38.317	1.00	0.00
ATOM	612	SG	CYS	78	43.910	25.711	39.967	1.00	0.00
ATOM	613	C	CYS	78	43.946	28.365	36.836	1.00	0.00
ATOM	614	O	CYS	78	44.834	29.211	36.751	1.00	0.00
ATOM	615	N	LEU	79	43.293	27.914	35.752	1.00	0.00
ATOM	616	CA	LEU	79	43.663	28.371	34.443	1.00	0.00
ATOM	617	CB	LEU	79	42.854	27.695	33.325	1.00	0.00
ATOM	618	CG	LEU	79	43.171	26.200	33.156	1.00	0.00
ATOM	619	CD2	LEU	79	44.680	25.969	32.963	1.00	0.00
ATOM	620	CD1	LEU	79	42.332	25.587	32.025	1.00	0.00
ATOM	621	C	LEU	79	43.427	29.848	34.334	1.00	0.00
ATOM	622	O	LEU	79	44.252	30.571	33.778	1.00	0.00
ATOM	623	N	SER	80	42.289	30.340	34.856	1.00	0.00
ATOM	624	CA	SER	80	41.946	31.730	34.721	1.00	0.00
ATOM	625	CB	SER	80	40.522	32.041	35.214	1.00	0.00
ATOM	626	OG	SER	80	39.568	31.365	34.408	1.00	0.00
ATOM	627	C	SER	80	42.881	32.614	35.489	1.00	0.00
ATOM	628	O	SER	80	43.304	33.653	34.986	1.00	0.00
ATOM	629	N	SER	81	43.217	32.241	36.737	1.00	0.00
ATOM	630	CA	SER	81	44.062	33.086	37.536	1.00	0.00
ATOM	631	CB	SER	81	44.198	32.596	38.989	1.00	0.00
ATOM	632	OG	SER	81	45.043	33.471	39.720	1.00	0.00
ATOM	633	C	SER	81	45.428	33.117	36.926	1.00	0.00
ATOM	634	O	SER	81	46.124	34.129	36.980	1.00	0.00
ATOM	635	N	PHE	82	45.847	31.986	36.334	1.00	0.00
ATOM	636	CA	PHE	82	47.141	31.861	35.731	1.00	0.00
ATOM	637	CB	PHE	82	47.375	30.406	35.273	1.00	0.00
ATOM	638	CG	PHE	82	48.827	30.155	35.056	1.00	0.00
ATOM	639	CD1	PHE	82	49.665	29.989	36.135	1.00	0.00
ATOM	640	CD2	PHE	82	49.346	30.051	33.788	1.00	0.00
ATOM	641	CE1	PHE	82	51.006	29.745	35.955	1.00	0.00
ATOM	642	CE2	PHE	82	50.686	29.807	33.601	1.00	0.00
ATOM	643	CZ	PHE	82	51.518	29.656	34.684	1.00	0.00
ATOM	644	C	PHE	82	47.185	32.781	34.545	1.00	0.00
ATOM	645	O	PHE	82	48.177	33.473	34.316	1.00	0.00
ATOM	646	N	ALA	83	46.092	32.801	33.755	1.00	0.00

	ATOM	647	CA	ALA	83	45.988	33.623	32.580	1.00	0.00
	ATOM	648	CB	ALA	83	44.678	33.392	31.807	1.00	0.00
	ATOM	649	C	ALA	83	46.026	35.065	32.978	1.00	0.00
	ATOM	650	O	ALA	83	46.677	35.883	32.329	1.00	0.00
5	ATOM	665	N	TRP	86	49.445	36.147	33.580	1.00	0.00
	ATOM	666	CA	TRP	86	50.241	36.360	32.408	1.00	0.00
	ATOM	667	CB	TRP	86	50.115	35.246	31.363	1.00	0.00
	ATOM	668	CG	TRP	86	51.048	35.483	30.206	1.00	0.00
	ATOM	669	CD2	TRP	86	52.475	35.422	30.336	1.00	0.00
10	ATOM	670	CD1	TRP	86	50.790	35.860	28.920	1.00	0.00
	ATOM	671	NE1	TRP	86	51.972	36.024	28.236	1.00	0.00
	ATOM	672	CE2	TRP	86	53.017	35.763	29.098	1.00	0.00
	ATOM	673	CE3	TRP	86	53.268	35.120	31.407	1.00	0.00
	ATOM	674	CZ2	TRP	86	54.369	35.806	28.910	1.00	0.00
15	ATOM	675	CZ3	TRP	86	54.629	35.153	31.211	1.00	0.00
	ATOM	676	CH2	TRP	86	55.169	35.489	29.986	1.00	0.00
	ATOM	677	C	TRP	86	49.916	37.667	31.747	1.00	0.00
	ATOM	678	O	TRP	86	50.815	38.401	31.343	1.00	0.00
	ATOM	679	N	ARG	87	48.619	37.999	31.615	1.00	0.00
20	ATOM	680	CA	ARG	87	48.224	39.208	30.946	1.00	0.00
	ATOM	681	CB	ARG	87	46.697	39.320	30.782	1.00	0.00
	ATOM	682	CG	ARG	87	46.177	38.518	29.583	1.00	0.00
	ATOM	683	CD	ARG	87	44.654	38.499	29.424	1.00	0.00
	ATOM	684	NE	ARG	87	44.130	37.261	30.072	1.00	0.00
25	ATOM	685	CZ	ARG	87	43.828	37.222	31.403	1.00	0.00
	ATOM	686	NH1	ARG	87	44.048	38.310	32.193	1.00	0.00
	ATOM	687	NH2	ARG	87	43.301	36.089	31.951	1.00	0.00
	ATOM	688	C	ARG	87	48.734	40.396	31.700	1.00	0.00
	ATOM	689	O	ARG	87	49.153	41.387	31.106	1.00	0.00
30	ATOM	708	N	LYS	90	52.507	40.704	31.086	1.00	0.00
	ATOM	709	CA	LYS	90	52.874	41.161	29.777	1.00	0.00
	ATOM	710	CB	LYS	90	52.219	40.305	28.682	1.00	0.00
	ATOM	711	CG	LYS	90	52.843	40.475	27.298	1.00	0.00
	ATOM	712	CD	LYS	90	52.458	39.344	26.345	1.00	0.00
35	ATOM	713	CE	LYS	90	53.062	39.476	24.949	1.00	0.00
	ATOM	714	NZ	LYS	90	52.710	38.287	24.142	1.00	0.00
	ATOM	715	C	LYS	90	52.528	42.598	29.508	1.00	0.00
	ATOM	716	O	LYS	90	53.366	43.358	29.023	1.00	0.00
	ATOM	717	N	HIS	91	51.258	42.989	29.744	1.00	0.00
40	ATOM	718	CA	HIS	91	50.834	44.320	29.395	1.00	0.00

ATOM	719	ND1	HIS	91	49.206	43.769	26.718	1.00	0.00
ATOM	720	CG	HIS	91	48.929	43.494	28.039	1.00	0.00
ATOM	721	NE2	HIS	91	48.198	41.788	26.757	1.00	0.00
ATOM	722	CD2	HIS	91	48.311	42.282	28.045	1.00	0.00
ATOM	723	CE1	HIS	91	48.749	42.716	25.996	1.00	0.00
ATOM	724	CB	HIS	91	49.316	44.393	29.172	1.00	0.00
ATOM	725	C	HIS	91	51.233	45.390	30.369	1.00	0.00
ATOM	726	O	HIS	91	51.759	46.435	29.998	1.00	0.00
ATOM	804	N	PRO	101	41.024	44.104	28.674	1.00	0.00
ATOM	805	CA	PRO	101	41.382	45.430	28.240	1.00	0.00
ATOM	806	CD	PRO	101	40.297	43.370	27.648	1.00	0.00
ATOM	807	CB	PRO	101	41.182	45.423	26.725	1.00	0.00
ATOM	808	CG	PRO	101	40.064	44.385	26.520	1.00	0.00
ATOM	809	C	PRO	101	40.491	46.456	28.882	1.00	0.00
ATOM	810	O	PRO	101	40.960	47.552	29.183	1.00	0.00
ATOM	1122	N	TYR	139	55.206	29.212	29.912	1.00	0.00
ATOM	1123	CA	TYR	139	53.880	29.563	30.334	1.00	0.00
ATOM	1124	CB	TYR	139	53.601	31.034	29.953	1.00	0.00
ATOM	1125	CG	TYR	139	52.188	31.433	30.200	1.00	0.00
ATOM	1126	CD1	TYR	139	51.726	31.666	31.474	1.00	0.00
ATOM	1127	CD2	TYR	139	51.332	31.609	29.138	1.00	0.00
ATOM	1128	CE1	TYR	139	50.420	32.046	31.682	1.00	0.00
ATOM	1129	CE2	TYR	139	50.027	31.990	29.338	1.00	0.00
ATOM	1130	CZ	TYR	139	49.569	32.207	30.614	1.00	0.00
ATOM	1131	OH	TYR	139	48.230	32.597	30.829	1.00	0.00
ATOM	1132	C	TYR	139	52.877	28.666	29.665	1.00	0.00
ATOM	1133	O	TYR	139	51.978	28.133	30.316	1.00	0.00
ATOM	1134	N	THR	140	53.023	28.451	28.344	1.00	0.00
ATOM	1135	CA	THR	140	52.065	27.679	27.603	1.00	0.00
ATOM	1136	CB	THR	140	52.355	27.654	26.126	1.00	0.00
ATOM	1137	OG1	THR	140	51.289	27.029	25.427	1.00	0.00
ATOM	1138	CG2	THR	140	53.675	26.906	25.874	1.00	0.00
ATOM	1139	C	THR	140	52.015	26.271	28.099	1.00	0.00
ATOM	1140	O	THR	140	50.942	25.684	28.227	1.00	0.00
ATOM	1157	N	LYS	143	50.485	26.019	31.567	1.00	0.00
ATOM	1158	CA	LYS	143	49.063	26.209	31.513	1.00	0.00
ATOM	1159	CB	LYS	143	48.652	27.022	30.271	1.00	0.00
ATOM	1160	CG	LYS	143	48.857	28.531	30.349	1.00	0.00
ATOM	1161	CD	LYS	143	47.776	29.256	31.147	1.00	0.00
ATOM	1162	CE	LYS	143	46.693	29.859	30.247	1.00	0.00

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ATOM   1163  NZ  LYS   143      46.140  28.822  29.343  1.00  0.00
ATOM   1164  C   LYS   143      48.410  24.876  31.309  1.00  0.00
ATOM   1165  O   LYS   143      47.403  24.565  31.944  1.00  0.00
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PPARgamma Site II Residues (ref. 2PRG.pdb)

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ATOM     93  N   TYR A 219      49.317 -20.485   0.542  1.00 26.16
ATOM     94  CA  TYR A 219      48.188 -21.396   0.545  1.00 27.09
ATOM     95  C   TYR A 219      48.474 -22.592  -0.357  1.00 28.21
ATOM     96  O   TYR A 219      48.164 -23.724   0.008  1.00 27.53
ATOM     97  CB  TYR A 219      46.909 -20.661   0.113  1.00 31.07
ATOM     98  CG  TYR A 219      45.667 -21.528   0.102  1.00 34.26
ATOM     99  CD1 TYR A 219      45.415 -22.424   1.135  1.00 30.92
ATOM    100  CD2 TYR A 219      44.724 -21.417  -0.912  1.00 37.77
ATOM    101  CE1 TYR A 219      44.256 -23.191   1.161  1.00 35.65
ATOM    102  CE2 TYR A 219      43.550 -22.181  -0.898  1.00 41.57
ATOM    103  CZ  TYR A 219      43.328 -23.066   0.144  1.00 38.33
ATOM    104  OH  TYR A 219      42.188 -23.837   0.171  1.00 42.57
ATOM    105  N   ASP A 220      49.086 -22.357  -1.519  1.00 30.62
ATOM    106  CA  ASP A 220      49.409 -23.473  -2.412  1.00 32.11
ATOM    107  C   ASP A 220      50.414 -24.436  -1.797  1.00 28.77
ATOM    108  O   ASP A 220      50.240 -25.652  -1.888  1.00 30.81
ATOM    109  CB  ASP A 220      49.983 -23.010  -3.758  1.00 31.77
ATOM    110  CG  ASP A 220      48.984 -22.238  -4.593  1.00 33.82
ATOM    111  OD1 ASP A 220      47.784 -22.586  -4.572  1.00 33.95
ATOM    112  OD2 ASP A 220      49.409 -21.301  -5.293  1.00 39.99
ATOM    113  N   SER A 221      51.466 -23.911  -1.175  1.00 29.83
ATOM    114  CA  SER A 221      52.467 -24.800  -0.597  1.00 32.70
ATOM    115  C   SER A 221      51.877 -25.501   0.616  1.00 28.79
ATOM    116  O   SER A 221      52.251 -26.623   0.938  1.00 31.65
ATOM    117  CB  SER A 221      53.743 -24.033  -0.231  1.00 33.22
ATOM    118  OG  SER A 221      53.502 -23.093   0.784  1.00 42.80
ATOM    119  N   TYR A 222      50.936 -24.834   1.275  1.00 32.44
ATOM    120  CA  TYR A 222      50.259 -25.415   2.424  1.00 29.27
ATOM    121  C   TYR A 222      49.438 -26.592   1.910  1.00 31.32
ATOM    122  O   TYR A 222      49.440 -27.661   2.517  1.00 33.08
ATOM    123  CB  TYR A 222      49.383 -24.347   3.091  1.00 29.11
ATOM    124  CG  TYR A 222      48.384 -24.814   4.128  1.00 23.58
ATOM    125  CD1 TYR A 222      47.233 -25.521   3.754  1.00 25.68
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ATOM	126	CD2	TYR	A	222	48.526	-24.449	5.471	1.00 27.50
ATOM	127	CE1	TYR	A	222	46.240	-25.839	4.690	1.00 31.92
ATOM	128	CE2	TYR	A	222	47.536	-24.762	6.422	1.00 24.65
ATOM	129	CZ	TYR	A	222	46.394	-25.452	6.022	1.00 30.90
ATOM	130	OH	TYR	A	222	45.392	-25.716	6.937	1.00 31.36
ATOM	131	N	ILE	A	223	48.751	-26.409	0.781	1.00 34.58
ATOM	132	CA	ILE	A	223	47.963	-27.502	0.208	1.00 34.35
ATOM	133	C	ILE	A	223	48.866	-28.678	-0.144	1.00 35.22
ATOM	134	O	ILE	A	223	48.477	-29.832	0.005	1.00 36.41
ATOM	135	CB	ILE	A	223	47.216	-27.088	-1.085	1.00 34.59
ATOM	136	CG1	ILE	A	223	46.071	-26.134	-0.754	1.00 35.22
ATOM	137	CG2	ILE	A	223	46.683	-28.340	-1.803	1.00 32.70
ATOM	138	CD1	ILE	A	223	45.010	-26.742	0.136	1.00 39.33
ATOM	139	N	LYS	A	224	50.073	-28.380	-0.619	1.00 36.65
ATOM	140	CA	LYS	A	224	51.011	-29.434	-0.989	1.00 38.16
ATOM	141	C	LYS	A	224	51.738	-30.133	0.144	1.00 34.79
ATOM	142	O	LYS	A	224	52.132	-31.284	-0.013	1.00 35.05
ATOM	143	CB	LYS	A	224	52.058	-28.914	-1.974	1.00 40.32
ATOM	144	CG	LYS	A	224	51.555	-28.828	-3.407	1.00 50.64
ATOM	145	CD	LYS	A	224	52.713	-28.647	-4.382	1.00 58.74
ATOM	146	CE	LYS	A	224	52.248	-28.792	-5.826	1.00 58.38
ATOM	147	NZ	LYS	A	224	53.382	-28.721	-6.790	1.00 62.48
ATOM	148	N	SER	A	225	51.893	-29.457	1.281	1.00 32.90
ATOM	149	CA	SER	A	225	52.631	-30.012	2.416	1.00 32.12
ATOM	150	C	SER	A	225	51.796	-30.776	3.433	1.00 33.07
ATOM	151	O	SER	A	225	52.283	-31.713	4.066	1.00 34.52
ATOM	152	CB	SER	A	225	53.380	-28.888	3.153	1.00 29.50
ATOM	153	OG	SER	A	225	54.250	-28.179	2.287	1.00 36.10
ATOM	154	N	PHE	A	226	50.540	-30.375	3.589	1.00 32.08
ATOM	155	CA	PHE	A	226	49.664	-30.994	4.565	1.00 34.40
ATOM	156	C	PHE	A	226	48.522	-31.784	3.935	1.00 39.63
ATOM	157	O	PHE	A	226	47.620	-31.215	3.326	1.00 41.93
ATOM	158	CB	PHE	A	226	49.106	-29.911	5.482	1.00 30.58
ATOM	159	CG	PHE	A	226	50.167	-29.043	6.108	1.00 30.45
ATOM	160	CD1	PHE	A	226	51.124	-29.591	6.958	1.00 26.08
ATOM	161	CD2	PHE	A	226	50.211	-27.674	5.844	1.00 32.25
ATOM	162	CE1	PHE	A	226	52.110	-28.790	7.535	1.00 26.05
ATOM	163	CE2	PHE	A	226	51.190	-26.864	6.415	1.00 31.29
ATOM	164	CZ	PHE	A	226	52.141	-27.423	7.261	1.00 33.33
ATOM	165	N	PRO	A	227	48.535	-33.113	4.107	1.00 44.70

ATOM	166	CA	PRO	A	227	47.529	-34.040	3.578	1.00 46.95
ATOM	167	C	PRO	A	227	46.124	-33.753	4.093	1.00 45.50
ATOM	168	O	PRO	A	227	45.189	-33.532	3.315	1.00 45.30
ATOM	169	CB	PRO	A	227	48.041	-35.398	4.062	1.00 46.06
ATOM	170	CG	PRO	A	227	49.531	-35.177	4.132	1.00 50.39
ATOM	171	CD	PRO	A	227	49.535	-33.868	4.879	1.00 47.37
ATOM	650	N	ARG	A	288	53.071	-39.607	15.013	1.00 47.42
ATOM	651	CA	ARG	A	288	52.383	-38.698	14.108	1.00 46.07
ATOM	652	C	ARG	A	288	53.036	-37.325	14.091	1.00 41.26
ATOM	653	O	ARG	A	288	52.933	-36.595	13.111	1.00 39.85
ATOM	654	CB	ARG	A	288	50.905	-38.573	14.496	1.00 50.86
ATOM	655	CG	ARG	A	288	50.176	-37.445	13.773	1.00 59.11
ATOM	656	CD	ARG	A	288	50.362	-37.533	12.261	1.00 65.80
ATOM	657	NE	ARG	A	288	50.009	-36.275	11.608	1.00 71.79
ATOM	658	CZ	ARG	A	288	50.278	-35.987	10.339	1.00 72.53
ATOM	659	NH1	ARG	A	288	50.905	-36.867	9.575	1.00 72.45
ATOM	660	NH2	ARG	A	288	49.931	-34.811	9.835	1.00 76.74
ATOM	661	N	SER	A	289	53.717	-36.986	15.180	1.00 41.14
ATOM	662	CA	SER	A	289	54.394	-35.702	15.296	1.00 38.47
ATOM	663	C	SER	A	289	55.675	-35.710	14.463	1.00 38.98
ATOM	664	O	SER	A	289	56.054	-34.694	13.884	1.00 38.45
ATOM	665	CB	SER	A	289	54.713	-35.416	16.764	1.00 39.42
ATOM	666	OG	SER	A	289	55.352	-34.163	16.909	1.00 46.15
ATOM	683	N	ALA	A	292	54.638	-34.991	11.179	1.00 42.33
ATOM	684	CA	ALA	A	292	54.244	-33.586	11.135	1.00 37.96
ATOM	685	C	ALA	A	292	55.461	-32.669	10.999	1.00 36.30
ATOM	686	O	ALA	A	292	55.425	-31.684	10.265	1.00 37.45
ATOM	687	CB	ALA	A	292	53.444	-33.229	12.386	1.00 31.14
ATOM	688	N	VAL	A	293	56.541	-32.993	11.703	1.00 37.86
ATOM	689	CA	VAL	A	293	57.759	-32.189	11.631	1.00 35.96
ATOM	690	C	VAL	A	293	58.276	-32.092	10.193	1.00 37.16
ATOM	691	O	VAL	A	293	58.750	-31.044	9.753	1.00 39.01
ATOM	692	CB	VAL	A	293	58.875	-32.795	12.503	1.00 32.38
ATOM	693	CG1	VAL	A	293	60.176	-32.003	12.320	1.00 30.77
ATOM	694	CG2	VAL	A	293	58.447	-32.798	13.951	1.00 32.30
ATOM	695	N	GLN	A	294	58.180	-33.198	9.467	1.00 36.25
ATOM	696	CA	GLN	A	294	58.649	-33.264	8.092	1.00 32.53
ATOM	697	C	GLN	A	294	57.780	-32.457	7.133	1.00 29.89
ATOM	698	O	GLN	A	294	58.289	-31.799	6.226	1.00 28.01
ATOM	699	CB	GLN	A	294	58.721	-34.730	7.673	1.00 36.86

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ATOM    700  CG  GLN A 294      59.677 -35.533   8.566  1.00 41.69
ATOM    701  CD  GLN A 294      59.618 -37.028   8.318  1.00 49.48
ATOM    702  OE1 GLN A 294      59.878 -37.503   7.210  1.00 52.48
ATOM    703  NE2 GLN A 294      59.276 -37.781   9.355  1.00 51.85
ATOM    704  N   GLU A 295      56.473 -32.495   7.342  1.00 26.58
ATOM    705  CA  GLU A 295      55.545 -31.756   6.498  1.00 29.65
ATOM    706  C   GLU A 295      55.713 -30.266   6.765  1.00 27.31
ATOM    707  O   GLU A 295      55.750 -29.461   5.834  1.00 28.65
ATOM    708  CB  GLU A 295      54.105 -32.164   6.816  1.00 31.76
ATOM    709  CG  GLU A 295      53.894 -33.662   6.874  1.00 41.29
ATOM    710  CD  GLU A 295      52.489 -34.037   7.311  1.00 43.08
ATOM    711  OE1 GLU A 295      51.992 -33.456   8.296  1.00 49.49
ATOM    712  OE2 GLU A 295      51.888 -34.931   6.685  1.00 52.62
ATOM    713  N   ILE A 296      55.815 -29.917   8.050  1.00 28.18
ATOM    714  CA  ILE A 296      55.973 -28.532   8.492  1.00 29.14
ATOM    715  C   ILE A 296      57.293 -27.927   8.036  1.00 30.82
ATOM    716  O   ILE A 296      57.362 -26.746   7.683  1.00 30.56
ATOM    717  CB  ILE A 296      55.890 -28.429  10.037  1.00 31.25
ATOM    718  CG1 ILE A 296      54.514 -28.906  10.508  1.00 33.48
ATOM    719  CG2 ILE A 296      56.121 -26.985  10.493  1.00 24.18
ATOM    720  CD1 ILE A 296      54.348 -28.908  12.015  1.00 34.47
ATOM    721  N   THR A 297      58.347 -28.731   8.056  1.00 32.77
ATOM    722  CA  THR A 297      59.648 -28.249   7.625  1.00 29.52
ATOM    723  C   THR A 297      59.612 -27.944   6.136  1.00 29.40
ATOM    724  O   THR A 297      60.193 -26.961   5.679  1.00 27.20
ATOM    725  CB  THR A 297      60.743 -29.282   7.902  1.00 30.55
ATOM    726  OG1 THR A 297      60.900 -29.435   9.321  1.00 31.64
ATOM    727  CG2 THR A 297      62.058 -28.841   7.261  1.00 29.15
ATOM    728  N   GLU A 298      58.926 -28.792   5.381  1.00 31.50
ATOM    729  CA  GLU A 298      58.810 -28.571   3.950  1.00 34.95
ATOM    730  C   GLU A 298      58.034 -27.268   3.735  1.00 32.29
ATOM    731  O   GLU A 298      58.417 -26.426   2.927  1.00 33.09
ATOM    732  CB  GLU A 298      58.079 -29.735   3.287  1.00 37.99
ATOM    733  CG  GLU A 298      58.301 -29.782   1.791  1.00 53.91
ATOM    734  CD  GLU A 298      59.779 -29.915   1.438  1.00 58.00
ATOM    735  OE1 GLU A 298      60.409 -30.919   1.837  1.00 66.07
ATOM    736  OE2 GLU A 298      60.312 -29.006   0.766  1.00 65.07
ATOM    737  N   TYR A 299      56.942 -27.095   4.468  1.00 31.49
ATOM    738  CA  TYR A 299      56.167 -25.872   4.346  1.00 26.31
ATOM    739  C   TYR A 299      57.009 -24.654   4.704  1.00 27.39
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ATOM    740  O   TYR A 299      56.949 -23.632   4.029  1.00 26.41
ATOM    741  CB  TYR A 299      54.961 -25.895   5.276  1.00 25.28
ATOM    742  CG  TYR A 299      54.183 -24.609   5.242  1.00 23.43
ATOM    743  CD1 TYR A 299      53.431 -24.262   4.117  1.00 24.14
ATOM    744  CD2 TYR A 299      54.232 -23.716   6.311  1.00 23.27
ATOM    745  CE1 TYR A 299      52.741 -23.054   4.052  1.00 24.89
ATOM    746  CE2 TYR A 299      53.548 -22.503   6.261  1.00 25.45
ATOM    747  CZ  TYR A 299      52.806 -22.183   5.126  1.00 25.47
ATOM    748  OH  TYR A 299      52.139 -20.991   5.058  1.00 29.93
ATOM    914  N   GLY A 321      58.998 -23.431  16.750  1.00 35.39
ATOM    915  CA  GLY A 321      57.701 -23.228  16.129  1.00 35.61
ATOM    916  C   GLY A 321      56.938 -24.471  15.728  1.00 33.20
ATOM    917  O   GLY A 321      55.727 -24.409  15.520  1.00 36.84
ATOM    918  N   VAL A 322      57.620 -25.604  15.623  1.00 32.05
ATOM    919  CA  VAL A 322      56.942 -26.823  15.208  1.00 32.49
ATOM    920  C   VAL A 322      55.750 -27.232  16.070  1.00 31.08
ATOM    921  O   VAL A 322      54.695 -27.574  15.536  1.00 36.08
ATOM    922  CB  VAL A 322      57.929 -28.011  15.101  1.00 37.63
ATOM    923  CG1 VAL A 322      57.163 -29.314  14.889  1.00 42.68
ATOM    924  CG2 VAL A 322      58.851 -27.796  13.912  1.00 38.13
ATOM    925  N   HIS A 323      55.891 -27.207  17.389  1.00 30.11
ATOM    926  CA  HIS A 323      54.754 -27.604  18.207  1.00 31.92
ATOM    927  C   HIS A 323      53.594 -26.624  18.194  1.00 29.54
ATOM    928  O   HIS A 323      52.441 -27.041  18.240  1.00 27.50
ATOM    929  CB  HIS A 323      55.172 -27.914  19.647  1.00 30.61
ATOM    930  CG  HIS A 323      55.918 -29.203  19.778  1.00 34.26
ATOM    931  ND1 HIS A 323      57.291 -29.267  19.870  1.00 37.08
ATOM    932  CD2 HIS A 323      55.481 -30.487  19.767  1.00 36.78
ATOM    933  CE1 HIS A 323      57.669 -30.533  19.909  1.00 37.36
ATOM    934  NE2 HIS A 323      56.590 -31.293  19.847  1.00 34.75
ATOM    935  N   GLU A 324      53.888 -25.329  18.119  1.00 30.21
ATOM    936  CA  GLU A 324      52.819 -24.340  18.084  1.00 27.19
ATOM    937  C   GLU A 324      51.993 -24.567  16.818  1.00 28.15
ATOM    938  O   GLU A 324      50.788 -24.324  16.797  1.00 28.90
ATOM    939  CB  GLU A 324      53.397 -22.923  18.099  1.00 24.17
ATOM    940  CG  GLU A 324      54.104 -22.559  19.399  1.00 26.67
ATOM    941  CD  GLU A 324      54.720 -21.166  19.374  1.00 29.48
ATOM    942  OE1 GLU A 324      54.533 -20.423  18.386  1.00 32.08
ATOM    943  OE2 GLU A 324      55.401 -20.808  20.353  1.00 29.74
ATOM    944  N   ILE A 325      52.650 -25.040  15.764  1.00 29.34
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ATOM	945	CA	ILE	A	325	51.969	-25.305	14.505	1.00 27.95
ATOM	946	C	ILE	A	325	51.235	-26.637	14.552	1.00 27.21
ATOM	947	O	ILE	A	325	50.156	-26.777	13.980	1.00 26.67
ATOM	948	CB	ILE	A	325	52.963	-25.308	13.319	1.00 29.47
ATOM	949	CG1	ILE	A	325	53.570	-23.910	13.169	1.00 31.96
ATOM	950	CG2	ILE	A	325	52.259	-25.746	12.023	1.00 26.17
ATOM	951	CD1	ILE	A	325	54.519	-23.798	12.016	1.00 36.43
ATOM	952	N	ILE	A	326	51.814	-27.620	15.236	1.00 26.54
ATOM	953	CA	ILE	A	326	51.157	-28.914	15.339	1.00 28.11
ATOM	954	C	ILE	A	326	49.825	-28.743	16.057	1.00 29.17
ATOM	955	O	ILE	A	326	48.798	-29.274	15.626	1.00 29.80
ATOM	956	CB	ILE	A	326	52.015	-29.929	16.118	1.00 33.05
ATOM	957	CG1	ILE	A	326	53.267	-30.281	15.306	1.00 31.62
ATOM	958	CG2	ILE	A	326	51.185	-31.184	16.445	1.00 27.50
ATOM	959	CD1	ILE	A	326	54.192	-31.278	15.993	1.00 29.00
ATOM	960	N	TYR	A	327	49.836	-27.981	17.145	1.00 29.50
ATOM	961	CA	TYR	A	327	48.620	-27.779	17.918	1.00 30.34
ATOM	962	C	TYR	A	327	47.612	-26.890	17.221	1.00 32.40
ATOM	963	O	TYR	A	327	46.413	-26.984	17.487	1.00 32.56
ATOM	964	CB	TYR	A	327	48.967	-27.246	19.310	1.00 29.71
ATOM	965	CG	TYR	A	327	49.845	-28.208	20.082	1.00 27.91
ATOM	966	CD1	TYR	A	327	49.495	-29.554	20.202	1.00 36.87
ATOM	967	CD2	TYR	A	327	51.028	-27.786	20.673	1.00 34.57
ATOM	968	CE1	TYR	A	327	50.312	-30.457	20.896	1.00 39.01
ATOM	969	CE2	TYR	A	327	51.850	-28.677	21.369	1.00 35.00
ATOM	970	CZ	TYR	A	327	51.488	-30.007	21.476	1.00 37.53
ATOM	971	OH	TYR	A	327	52.289	-30.885	22.176	1.00 43.90
ATOM	972	N	THR	A	328	48.097	-26.033	16.321	1.00 33.44
ATOM	973	CA	THR	A	328	47.217	-25.159	15.556	1.00 27.97
ATOM	974	C	THR	A	328	46.500	-26.030	14.526	1.00 28.13
ATOM	975	O	THR	A	328	45.289	-25.925	14.341	1.00 28.36
ATOM	976	CB	THR	A	328	48.015	-24.062	14.803	1.00 31.65
ATOM	977	OG1	THR	A	328	48.614	-23.166	15.749	1.00 34.24
ATOM	978	CG2	THR	A	328	47.100	-23.279	13.857	1.00 28.42
ATOM	979	N	MET	A	329	47.268	-26.894	13.866	1.00 26.24
ATOM	980	CA	MET	A	329	46.740	-27.792	12.841	1.00 28.47
ATOM	981	C	MET	A	329	45.831	-28.853	13.461	1.00 30.21
ATOM	982	O	MET	A	329	44.822	-29.251	12.867	1.00 29.30
ATOM	983	CB	MET	A	329	47.893	-28.484	12.097	1.00 31.16
ATOM	984	CG	MET	A	329	48.870	-27.530	11.390	1.00 40.71

ATOM	985	SD	MET	A	329	48.138	-26.605	10.026	1.00 47.88
ATOM	986	CE	MET	A	329	47.820	-27.914	8.823	1.00 46.75
ATOM	1000	N	SER	A	332	42.137	-28.210	13.823	1.00 33.69
ATOM	1001	CA	SER	A	332	41.327	-28.455	12.634	1.00 31.46
ATOM	1002	C	SER	A	332	40.688	-29.850	12.678	1.00 34.05
ATOM	1003	O	SER	A	332	39.633	-30.071	12.093	1.00 36.02
ATOM	1004	CB	SER	A	332	42.180	-28.342	11.355	1.00 32.80
ATOM	1005	OG	SER	A	332	42.678	-27.026	11.143	1.00 34.02
ATOM	1006	N	LEU	A	333	41.326	-30.786	13.375	1.00 31.60
ATOM	1007	CA	LEU	A	333	40.827	-32.157	13.445	1.00 35.66
ATOM	1008	C	LEU	A	333	39.978	-32.399	14.688	1.00 33.42
ATOM	1009	O	LEU	A	333	39.483	-33.504	14.909	1.00 38.08
ATOM	1010	CB	LEU	A	333	42.009	-33.136	13.436	1.00 33.49
ATOM	1011	CG	LEU	A	333	43.111	-32.826	12.407	1.00 39.04
ATOM	1012	CD1	LEU	A	333	44.221	-33.875	12.471	1.00 30.81
ATOM	1013	CD2	LEU	A	333	42.513	-32.777	11.024	1.00 34.79
ATOM	1022	N	ASN	A	335	36.759	-31.278	17.509	1.00 37.06
ATOM	1023	CA	ASN	A	335	35.499	-30.613	17.799	1.00 34.66
ATOM	1024	C	ASN	A	335	35.479	-30.749	19.317	1.00 37.43
ATOM	1025	O	ASN	A	335	36.424	-31.309	19.896	1.00 36.55
ATOM	1026	CB	ASN	A	335	34.268	-31.269	17.141	1.00 36.33
ATOM	1027	CG	ASN	A	335	34.033	-32.694	17.578	1.00 33.81
ATOM	1028	OD1	ASN	A	335	34.175	-33.041	18.750	1.00 39.06
ATOM	1029	ND2	ASN	A	335	33.625	-33.526	16.635	1.00 41.11
ATOM	1030	N	LYS	A	336	34.438	-30.251	19.973	1.00 40.23
ATOM	1031	CA	LYS	A	336	34.385	-30.315	21.431	1.00 43.15
ATOM	1032	C	LYS	A	336	34.401	-31.726	22.021	1.00 43.02
ATOM	1033	O	LYS	A	336	34.794	-31.908	23.177	1.00 44.52
ATOM	1034	CB	LYS	A	336	33.144	-29.579	21.951	1.00 49.47
ATOM	1035	CG	LYS	A	336	31.832	-30.233	21.565	1.00 56.12
ATOM	1036	CD	LYS	A	336	30.654	-29.497	22.174	1.00 63.31
ATOM	1037	CE	LYS	A	336	29.347	-30.208	21.859	1.00 68.69
ATOM	1038	NZ	LYS	A	336	28.183	-29.551	22.517	1.00 72.75
ATOM	1080	N	GLU	A	343	44.675	-40.220	9.810	1.00 50.51
ATOM	1081	CA	GLU	A	343	44.295	-39.491	8.604	1.00 51.89
ATOM	1082	C	GLU	A	343	42.791	-39.468	8.328	1.00 50.95
ATOM	1083	O	GLU	A	343	42.363	-39.622	7.184	1.00 50.39
ATOM	1084	CB	GLU	A	343	45.027	-40.082	7.397	1.00 59.73
ATOM	1085	CG	GLU	A	343	46.541	-40.019	7.508	1.00 68.39
ATOM	1086	CD	GLU	A	343	47.240	-40.616	6.302	1.00 76.46

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ATOM   1087  OE1 GLU A 343      47.070 -41.832   6.049  1.00 78.36
ATOM   1088  OE2 GLU A 343      47.959 -39.865   5.605  1.00 79.29
ATOM   1419  N   LEU A 384      44.818 -20.042   7.630  1.00 27.46
ATOM   1420  CA  LEU A 384      45.776 -20.800   8.417  1.00 27.85
ATOM   1421  C   LEU A 384      47.169 -20.825   7.787  1.00 28.31
ATOM   1422  O   LEU A 384      48.173 -20.663   8.478  1.00 27.17
ATOM   1423  CB  LEU A 384      45.259 -22.228   8.617  1.00 25.10
ATOM   1424  CG  LEU A 384      43.996 -22.358   9.483  1.00 28.35
ATOM   1425  CD1 LEU A 384      43.482 -23.776   9.427  1.00 25.74
ATOM   1426  CD2 LEU A 384      44.306 -21.947  10.934  1.00 24.70
ATOM   1427  N   ALA A 385      47.237 -21.012   6.474  1.00 28.77
ATOM   1428  CA  ALA A 385      48.541 -21.054   5.815  1.00 28.21
ATOM   1429  C   ALA A 385      49.392 -19.832   6.154  1.00 23.50
ATOM   1430  O   ALA A 385      50.584 -19.968   6.393  1.00 28.41
ATOM   1431  CB  ALA A 385      48.373 -21.184   4.316  1.00 22.62
ATOM   1451  N   ILE A 388      50.323 -19.739  10.091  1.00 25.45
ATOM   1452  CA  ILE A 388      51.389 -20.683  10.388  1.00 25.58
ATOM   1453  C   ILE A 388      52.741 -20.079  10.026  1.00 23.26
ATOM   1454  O   ILE A 388      53.724 -20.295  10.720  1.00 30.01
ATOM   1455  CB  ILE A 388      51.169 -22.004   9.601  1.00 29.97
ATOM   1456  CG1 ILE A 388      49.853 -22.647  10.042  1.00 38.36
ATOM   1457  CG2 ILE A 388      52.316 -22.947   9.804  1.00 36.50
ATOM   1458  CD1 ILE A 388      49.736 -22.823  11.518  1.00 31.88
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PR Site II Residues (ref. 1A28.pdb)

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ATOM     76  N   MET A 692      27.562   5.259  83.253  1.00 24.62
ATOM     77  CA  MET A 692      26.351   4.476  83.019  1.00 27.60
ATOM     78  C   MET A 692      25.156   5.337  83.440  1.00 27.94
ATOM     79  O   MET A 692      24.145   5.416  82.745  1.00 25.86
ATOM     80  CB  MET A 692      26.385   3.195  83.860  1.00 27.45
ATOM     81  CG  MET A 692      25.197   2.289  83.686  1.00 39.52
ATOM     82  SD  MET A 692      25.017   1.642  82.004  1.00 51.06
ATOM     83  CE  MET A 692      24.268   3.029  81.134  1.00 52.36
ATOM     84  N   SER A 693      25.296   6.010  84.574  1.00 25.24
ATOM     85  CA  SER A 693      24.216   6.835  85.083  1.00 31.97
ATOM     86  C   SER A 693      23.878   8.044  84.219  1.00 29.88
ATOM     87  O   SER A 693      22.719   8.455  84.157  1.00 28.14
ATOM     88  CB  SER A 693      24.531   7.313  86.508  1.00 38.05
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ATOM	89	OG	SER	A	693	25.623	8.222	86.526	1.00	43.01
ATOM	90	N	ILE	A	694	24.865	8.625	83.547	1.00	25.23
ATOM	91	CA	ILE	A	694	24.553	9.808	82.741	1.00	26.22
ATOM	92	C	ILE	A	694	24.257	9.520	81.279	1.00	23.06
ATOM	93	O	ILE	A	694	24.031	10.442	80.504	1.00	24.41
ATOM	94	CB	ILE	A	694	25.669	10.875	82.813	1.00	22.83
ATOM	95	CG1	ILE	A	694	26.984	10.307	82.265	1.00	22.20
ATOM	96	CG2	ILE	A	694	25.849	11.338	84.270	1.00	28.20
ATOM	97	CD1	ILE	A	694	28.060	11.373	82.014	1.00	22.62
ATOM	98	N	GLU	A	695	24.257	8.242	80.899	1.00	26.89
ATOM	99	CA	GLU	A	695	23.969	7.876	79.517	1.00	21.93
ATOM	100	C	GLU	A	695	22.511	8.296	79.289	1.00	28.96
ATOM	101	O	GLU	A	695	21.632	7.992	80.087	1.00	29.21
ATOM	102	CB	GLU	A	695	24.150	6.362	79.338	1.00	34.17
ATOM	103	CG	GLU	A	695	24.063	5.848	77.911	1.00	34.86
ATOM	104	CD	GLU	A	695	25.240	6.232	77.021	1.00	45.46
ATOM	105	OE1	GLU	A	695	26.126	7.019	77.436	1.00	31.19
ATOM	106	OE2	GLU	A	695	25.275	5.730	75.873	1.00	49.30
ATOM	107	N	PRO	A	696	22.242	9.037	78.215	1.00	32.33
ATOM	108	CA	PRO	A	696	20.865	9.469	77.961	1.00	34.70
ATOM	109	C	PRO	A	696	19.862	8.330	77.764	1.00	30.39
ATOM	110	O	PRO	A	696	20.232	7.235	77.371	1.00	27.63
ATOM	111	CB	PRO	A	696	21.020	10.333	76.710	1.00	38.27
ATOM	112	CG	PRO	A	696	22.198	9.652	75.997	1.00	40.07
ATOM	113	CD	PRO	A	696	23.141	9.561	77.173	1.00	34.72
ATOM	114	N	ASP	A	697	18.588	8.613	78.037	1.00	38.27
ATOM	115	CA	ASP	A	697	17.516	7.632	77.863	1.00	35.46
ATOM	116	C	ASP	A	697	17.341	7.513	76.340	1.00	35.96
ATOM	117	O	ASP	A	697	17.600	8.468	75.620	1.00	30.43
ATOM	118	CB	ASP	A	697	16.238	8.147	78.523	1.00	44.25
ATOM	119	CG	ASP	A	697	15.176	7.069	78.683	1.00	53.62
ATOM	120	OD1	ASP	A	697	15.420	5.901	78.302	1.00	57.04
ATOM	121	OD2	ASP	A	697	14.085	7.398	79.203	1.00	61.97
ATOM	122	N	VAL	A	698	16.909	6.359	75.841	1.00	32.80
ATOM	123	CA	VAL	A	698	16.766	6.195	74.393	1.00	34.66
ATOM	124	C	VAL	A	698	15.941	7.312	73.736	1.00	28.44
ATOM	125	O	VAL	A	698	14.937	7.775	74.266	1.00	30.11
ATOM	126	CB	VAL	A	698	16.153	4.813	74.026	1.00	41.68
ATOM	127	CG1	VAL	A	698	14.649	4.830	74.237	1.00	38.06
ATOM	128	CG2	VAL	A	698	16.517	4.451	72.586	1.00	45.80

ATOM	282	N	LEU	A	721	16.006	12.741	63.995	1.00 19.58
ATOM	283	CA	LEU	A	721	16.568	11.942	65.084	1.00 17.13
ATOM	284	C	LEU	A	721	17.924	12.545	65.476	1.00 16.29
ATOM	285	O	LEU	A	721	18.228	12.690	66.662	1.00 19.55
ATOM	286	CB	LEU	A	721	16.742	10.479	64.638	1.00 17.00
ATOM	287	CG	LEU	A	721	17.378	9.549	65.673	1.00 19.10
ATOM	288	CD1	LEU	A	721	16.508	9.497	66.942	1.00 18.65
ATOM	289	CD2	LEU	A	721	17.536	8.145	65.037	1.00 17.08
ATOM	290	N	GLY	A	722	18.724	12.896	64.476	1.00 16.83
ATOM	291	CA	GLY	A	722	20.036	13.486	64.710	1.00 17.42
ATOM	292	C	GLY	A	722	19.929	14.774	65.516	1.00 24.76
ATOM	293	O	GLY	A	722	20.749	15.038	66.402	1.00 19.56
ATOM	314	N	GLN	A	725	19.296	13.770	69.009	1.00 19.77
ATOM	315	CA	GLN	A	725	20.474	13.188	69.634	1.00 19.30
ATOM	316	C	GLN	A	725	21.545	14.239	69.906	1.00 21.49
ATOM	317	O	GLN	A	725	22.309	14.113	70.855	1.00 21.43
ATOM	318	CB	GLN	A	725	21.055	12.063	68.771	1.00 19.47
ATOM	319	CG	GLN	A	725	20.135	10.843	68.774	1.00 22.41
ATOM	320	CD	GLN	A	725	20.746	9.633	68.092	1.00 30.53
ATOM	321	OE1	GLN	A	725	20.104	8.578	67.970	1.00 32.93
ATOM	322	NE2	GLN	A	725	21.987	9.770	67.647	1.00 27.09
ATOM	323	N	LEU	A	726	21.592	15.284	69.085	1.00 21.82
ATOM	324	CA	LEU	A	726	22.573	16.347	69.288	1.00 22.79
ATOM	325	C	LEU	A	726	22.284	17.027	70.624	1.00 21.40
ATOM	326	O	LEU	A	726	23.207	17.293	71.406	1.00 23.41
ATOM	327	CB	LEU	A	726	22.526	17.367	68.135	1.00 19.53
ATOM	328	CG	LEU	A	726	23.533	18.531	68.138	1.00 24.90
ATOM	329	CD1	LEU	A	726	24.948	18.005	68.300	1.00 22.88
ATOM	330	CD2	LEU	A	726	23.421	19.325	66.812	1.00 20.28
ATOM	331	N	LEU	A	727	21.007	17.301	70.890	1.00 18.00
ATOM	332	CA	LEU	A	727	20.623	17.906	72.156	1.00 19.91
ATOM	333	C	LEU	A	727	21.078	16.978	73.281	1.00 24.23
ATOM	334	O	LEU	A	727	21.678	17.402	74.274	1.00 19.07
ATOM	335	CB	LEU	A	727	19.105	18.065	72.247	1.00 21.64
ATOM	336	CG	LEU	A	727	18.591	18.563	73.594	1.00 21.40
ATOM	337	CD1	LEU	A	727	19.256	19.906	73.912	1.00 26.36
ATOM	338	CD2	LEU	A	727	17.082	18.699	73.546	1.00 28.00
ATOM	339	N	SER	A	728	20.783	15.695	73.106	1.00 21.94
ATOM	340	CA	SER	A	728	21.131	14.690	74.097	1.00 21.38
ATOM	341	C	SER	A	728	22.637	14.682	74.355	1.00 20.10

ATOM	342	O	SER	A	728	23.066	14.611	75.512	1.00 22.32
ATOM	343	CB	SER	A	728	20.645	13.310	73.630	1.00 24.08
ATOM	344	OG	SER	A	728	20.719	12.380	74.689	1.00 30.43
ATOM	345	N	VAL	A	729	23.433	14.741	73.297	1.00 18.72
ATOM	346	CA	VAL	A	729	24.891	14.781	73.415	1.00 20.27
ATOM	347	C	VAL	A	729	25.388	15.988	74.203	1.00 18.31
ATOM	348	O	VAL	A	729	26.274	15.860	75.049	1.00 19.16
ATOM	349	CB	VAL	A	729	25.574	14.796	72.034	1.00 17.15
ATOM	350	CG1	VAL	A	729	27.060	15.147	72.164	1.00 20.31
ATOM	351	CG2	VAL	A	729	25.453	13.395	71.407	1.00 21.83
ATOM	352	N	VAL	A	730	24.830	17.159	73.937	1.00 17.43
ATOM	353	CA	VAL	A	730	25.282	18.333	74.660	1.00 21.44
ATOM	354	C	VAL	A	730	24.888	18.225	76.132	1.00 19.86
ATOM	355	O	VAL	A	730	25.678	18.584	76.993	1.00 21.47
ATOM	356	CB	VAL	A	730	24.725	19.630	74.038	1.00 20.22
ATOM	357	CG1	VAL	A	730	25.210	20.849	74.834	1.00 21.24
ATOM	358	CG2	VAL	A	730	25.178	19.734	72.596	1.00 19.32
ATOM	359	N	LYS	A	731	23.686	17.727	76.427	1.00 17.73
ATOM	360	CA	LYS	A	731	23.275	17.552	77.817	1.00 22.58
ATOM	361	C	LYS	A	731	24.186	16.546	78.517	1.00 23.23
ATOM	362	O	LYS	A	731	24.613	16.757	79.659	1.00 20.64
ATOM	363	CB	LYS	A	731	21.808	17.121	77.911	1.00 23.07
ATOM	364	CG	LYS	A	731	20.850	18.296	77.646	1.00 25.92
ATOM	365	CD	LYS	A	731	19.388	18.009	78.016	1.00 37.08
ATOM	366	CE	LYS	A	731	18.717	17.034	77.063	1.00 48.50
ATOM	367	NZ	LYS	A	731	17.247	16.901	77.346	1.00 49.18
ATOM	368	N	TRP	A	732	24.486	15.452	77.828	1.00 18.73
ATOM	369	CA	TRP	A	732	25.383	14.437	78.364	1.00 21.37
ATOM	370	C	TRP	A	732	26.743	15.038	78.703	1.00 22.20
ATOM	371	O	TRP	A	732	27.293	14.772	79.770	1.00 23.93
ATOM	372	CB	TRP	A	732	25.552	13.321	77.334	1.00 21.47
ATOM	373	CG	TRP	A	732	26.674	12.347	77.582	1.00 17.78
ATOM	374	CD1	TRP	A	732	26.728	11.348	78.528	1.00 20.71
ATOM	375	CD2	TRP	A	732	27.861	12.225	76.806	1.00 17.23
ATOM	376	NE1	TRP	A	732	27.879	10.613	78.370	1.00 19.88
ATOM	377	CE2	TRP	A	732	28.593	11.130	77.318	1.00 19.41
ATOM	378	CE3	TRP	A	732	28.383	12.938	75.713	1.00 19.83
ATOM	379	CZ2	TRP	A	732	29.824	10.726	76.771	1.00 18.15
ATOM	380	CZ3	TRP	A	732	29.612	12.533	75.165	1.00 20.23
ATOM	381	CH2	TRP	A	732	30.314	11.435	75.701	1.00 22.27

ATOM	382	N	SER A 733	27.274	15.872	77.811	1.00	20.68
ATOM	555	N	SER A 754	33.038	15.988	66.904	1.00	19.69
ATOM	556	CA	SER A 754	32.699	14.594	67.147	1.00	21.05
ATOM	557	C	SER A 754	31.265	14.109	67.119	1.00	20.67
ATOM	558	O	SER A 754	31.042	12.893	67.259	1.00	17.40
ATOM	559	CB	SER A 754	33.288	14.196	68.498	1.00	24.21
ATOM	560	OG	SER A 754	32.556	14.827	69.535	1.00	27.35
ATOM	561	N	TRP A 755	30.300	14.998	66.911	1.00	17.55
ATOM	562	CA	TRP A 755	28.912	14.547	66.960	1.00	21.93
ATOM	563	C	TRP A 755	28.620	13.345	66.055	1.00	18.91
ATOM	564	O	TRP A 755	27.956	12.409	66.486	1.00	20.07
ATOM	565	CB	TRP A 755	27.925	15.684	66.647	1.00	22.52
ATOM	566	CG	TRP A 755	28.003	16.222	65.257	1.00	23.08
ATOM	567	CD1	TRP A 755	28.859	17.175	64.791	1.00	28.21
ATOM	568	CD2	TRP A 755	27.217	15.803	64.141	1.00	24.51
ATOM	569	NE1	TRP A 755	28.655	17.379	63.445	1.00	25.19
ATOM	570	CE2	TRP A 755	27.651	16.548	63.022	1.00	26.64
ATOM	571	CE3	TRP A 755	26.189	14.869	63.979	1.00	25.75
ATOM	572	CZ2	TRP A 755	27.089	16.388	61.743	1.00	29.86
ATOM	573	CZ3	TRP A 755	25.630	14.707	62.707	1.00	32.59
ATOM	574	CH2	TRP A 755	26.083	15.465	61.608	1.00	30.85
ATOM	575	N	MET A 756	29.114	13.357	64.820	1.00	21.38
ATOM	576	CA	MET A 756	28.848	12.243	63.896	1.00	18.69
ATOM	577	C	MET A 756	29.439	10.939	64.415	1.00	23.20
ATOM	578	O	MET A 756	28.794	9.878	64.350	1.00	21.19
ATOM	579	CB	MET A 756	29.432	12.529	62.511	1.00	21.49
ATOM	580	CG	MET A 756	29.112	11.430	61.496	1.00	22.22
ATOM	581	SD	MET A 756	27.367	11.449	60.920	1.00	27.03
ATOM	582	CE	MET A 756	27.451	12.902	59.772	1.00	26.64
ATOM	583	N	SER A 757	30.675	11.013	64.899	1.00	19.23
ATOM	584	CA	SER A 757	31.344	9.845	65.451	1.00	22.32
ATOM	585	C	SER A 757	30.575	9.283	66.631	1.00	20.68
ATOM	586	O	SER A 757	30.376	8.078	66.718	1.00	21.09
ATOM	587	CB	SER A 757	32.759	10.190	65.911	1.00	23.54
ATOM	588	OG	SER A 757	33.562	10.611	64.826	1.00	31.88
ATOM	589	N	LEU A 758	30.150	10.149	67.548	1.00	20.06
ATOM	590	CA	LEU A 758	29.430	9.698	68.735	1.00	16.39
ATOM	591	C	LEU A 758	28.105	9.061	68.355	1.00	18.68
ATOM	592	O	LEU A 758	27.709	8.038	68.918	1.00	18.94
ATOM	593	CB	LEU A 758	29.147	10.880	69.675	1.00	14.15

ATOM	594	CG	LEU	A	758	30.373	11.599	70.232	1.00 20.53
ATOM	595	CD1	LEU	A	758	29.919	12.855	70.981	1.00 20.07
ATOM	596	CD2	LEU	A	758	31.121	10.656	71.186	1.00 24.11
ATOM	597	N	MET	A	759	27.410	9.674	67.404	1.00 18.42
ATOM	598	CA	MET	A	759	26.125	9.149	67.001	1.00 19.21
ATOM	599	C	MET	A	759	26.209	7.828	66.242	1.00 19.93
ATOM	600	O	MET	A	759	25.363	6.949	66.456	1.00 23.09
ATOM	601	CB	MET	A	759	25.364	10.197	66.193	1.00 21.20
ATOM	602	CG	MET	A	759	24.937	11.397	67.065	1.00 21.45
ATOM	603	SD	MET	A	759	23.950	12.587	66.168	1.00 25.97
ATOM	604	CE	MET	A	759	23.941	13.961	67.348	1.00 26.52
ATOM	605	N	VAL	A	760	27.193	7.673	65.365	1.00 18.66
ATOM	606	CA	VAL	A	760	27.300	6.397	64.638	1.00 19.71
ATOM	607	C	VAL	A	760	27.779	5.292	65.596	1.00 22.38
ATOM	608	O	VAL	A	760	27.409	4.127	65.448	1.00 18.63
ATOM	609	CB	VAL	A	760	28.262	6.492	63.417	1.00 20.60
ATOM	610	CG1	VAL	A	760	29.708	6.659	63.860	1.00 22.90
ATOM	611	CG2	VAL	A	760	28.129	5.226	62.559	1.00 22.05
ATOM	612	N	PHE	A	761	28.597	5.672	66.572	1.00 18.16
ATOM	613	CA	PHE	A	761	29.107	4.729	67.579	1.00 20.65
ATOM	614	C	PHE	A	761	27.907	4.256	68.419	1.00 21.25
ATOM	615	O	PHE	A	761	27.773	3.058	68.717	1.00 23.39
ATOM	616	CB	PHE	A	761	30.166	5.441	68.447	1.00 19.84
ATOM	617	CG	PHE	A	761	31.100	4.502	69.206	1.00 22.22
ATOM	618	CD1	PHE	A	761	31.944	3.631	68.520	1.00 22.72
ATOM	619	CD2	PHE	A	761	31.158	4.529	70.597	1.00 23.08
ATOM	620	CE1	PHE	A	761	32.834	2.802	69.200	1.00 23.74
ATOM	621	CE2	PHE	A	761	32.044	3.706	71.297	1.00 24.95
ATOM	622	CZ	PHE	A	761	32.880	2.842	70.602	1.00 22.67
ATOM	623	N	GLY	A	762	27.041	5.196	68.803	1.00 18.00
ATOM	624	CA	GLY	A	762	25.851	4.861	69.564	1.00 19.15
ATOM	625	C	GLY	A	762	24.928	3.957	68.761	1.00 19.60
ATOM	626	O	GLY	A	762	24.304	3.038	69.306	1.00 17.94
ATOM	639	N	TRP	A	765	26.279	0.520	68.998	1.00 18.65
ATOM	640	CA	TRP	A	765	25.954	-0.118	70.265	1.00 21.70
ATOM	641	C	TRP	A	765	24.485	-0.582	70.330	1.00 20.69
ATOM	642	O	TRP	A	765	24.202	-1.710	70.730	1.00 20.73
ATOM	643	CB	TRP	A	765	26.275	0.832	71.426	1.00 19.80
ATOM	644	CG	TRP	A	765	25.985	0.232	72.766	1.00 20.60
ATOM	645	CD1	TRP	A	765	24.895	0.450	73.543	1.00 26.35

ATOM	646	CD2	TRP	A	765	26.765	-0.770	73.435	1.00 22.75
ATOM	647	NE1	TRP	A	765	24.936	-0.354	74.660	1.00 25.80
ATOM	648	CE2	TRP	A	765	26.076	-1.114	74.618	1.00 27.72
ATOM	649	CE3	TRP	A	765	27.974	-1.408	73.145	1.00 24.76
ATOM	650	CZ2	TRP	A	765	26.558	-2.080	75.522	1.00 28.33
ATOM	651	CZ3	TRP	A	765	28.461	-2.372	74.045	1.00 25.79
ATOM	652	CH2	TRP	A	765	27.747	-2.692	75.217	1.00 23.99
ATOM	653	N	ARG	A	766	23.544	0.273	69.936	1.00 20.81
ATOM	654	CA	ARG	A	766	22.136	-0.116	69.987	1.00 18.86
ATOM	655	C	ARG	A	766	21.844	-1.288	69.048	1.00 18.44
ATOM	656	O	ARG	A	766	21.066	-2.185	69.381	1.00 20.30
ATOM	657	CB	ARG	A	766	21.223	1.061	69.624	1.00 18.28
ATOM	658	CG	ARG	A	766	21.246	2.229	70.632	1.00 20.05
ATOM	659	CD	ARG	A	766	20.179	3.260	70.256	1.00 25.08
ATOM	660	NE	ARG	A	766	20.413	3.889	68.956	1.00 20.13
ATOM	661	CZ	ARG	A	766	21.239	4.908	68.742	1.00 22.33
ATOM	662	NH1	ARG	A	766	21.909	5.442	69.754	1.00 22.73
ATOM	663	NH2	ARG	A	766	21.380	5.412	67.519	1.00 19.31
ATOM	682	N	LYS	A	769	23.313	-4.427	70.751	1.00 19.61
ATOM	683	CA	LYS	A	769	22.500	-4.833	71.899	1.00 20.88
ATOM	684	C	LYS	A	769	21.090	-5.323	71.636	1.00 25.83
ATOM	685	O	LYS	A	769	20.661	-6.320	72.222	1.00 23.20
ATOM	686	CB	LYS	A	769	22.402	-3.682	72.904	1.00 26.26
ATOM	687	CG	LYS	A	769	23.682	-3.356	73.623	1.00 29.74
ATOM	688	CD	LYS	A	769	23.998	-4.345	74.756	1.00 34.33
ATOM	689	CE	LYS	A	769	23.010	-4.251	75.914	1.00 31.35
ATOM	690	NZ	LYS	A	769	23.424	-5.118	77.078	1.00 27.64
ATOM	691	N	HIS	A	770	20.372	-4.627	70.762	1.00 20.34
ATOM	692	CA	HIS	A	770	18.968	-4.935	70.496	1.00 25.32
ATOM	693	C	HIS	A	770	18.652	-5.887	69.353	1.00 24.30
ATOM	694	O	HIS	A	770	17.631	-6.572	69.382	1.00 23.64
ATOM	695	CB	HIS	A	770	18.204	-3.622	70.246	1.00 25.43
ATOM	696	CG	HIS	A	770	18.239	-2.672	71.397	1.00 32.32
ATOM	697	ND1	HIS	A	770	17.517	-2.879	72.554	1.00 34.84
ATOM	698	CD2	HIS	A	770	18.920	-1.516	71.581	1.00 28.95
ATOM	699	CE1	HIS	A	770	17.751	-1.889	73.398	1.00 36.65
ATOM	700	NE2	HIS	A	770	18.598	-1.049	72.833	1.00 35.04
ATOM	771	N	PRO	A	780	14.074	3.224	68.501	1.00 24.08
ATOM	772	CA	PRO	A	780	13.061	2.176	68.645	1.00 22.75
ATOM	773	C	PRO	A	780	11.985	2.260	67.551	1.00 31.17

ATOM	774	O	PRO	A	780	11.405	1.242	67.163	1.00 27.19
ATOM	775	CB	PRO	A	780	12.506	2.451	70.039	1.00 23.42
ATOM	776	CG	PRO	A	780	13.723	3.011	70.760	1.00 29.68
ATOM	777	CD	PRO	A	780	14.122	4.036	69.731	1.00 19.66
ATOM	1091	N	PHE	A	818	32.469	0.119	76.224	1.00 21.31
ATOM	1092	CA	PHE	A	818	31.805	1.043	75.304	1.00 22.08
ATOM	1093	C	PHE	A	818	31.696	2.467	75.884	1.00 21.29
ATOM	1094	O	PHE	A	818	31.920	3.460	75.180	1.00 20.03
ATOM	1095	CB	PHE	A	818	30.406	0.528	75.002	1.00 23.06
ATOM	1096	CG	PHE	A	818	29.513	1.549	74.373	1.00 22.01
ATOM	1097	CD1	PHE	A	818	29.678	1.914	73.040	1.00 22.32
ATOM	1098	CD2	PHE	A	818	28.514	2.156	75.124	1.00 23.62
ATOM	1099	CE1	PHE	A	818	28.852	2.869	72.467	1.00 27.65
ATOM	1100	CE2	PHE	A	818	27.681	3.116	74.558	1.00 28.88
ATOM	1101	CZ	PHE	A	818	27.852	3.471	73.231	1.00 22.16
ATOM	1102	N	LEU	A	819	31.323	2.556	77.154	1.00 21.31
ATOM	1103	CA	LEU	A	819	31.164	3.857	77.812	1.00 23.49
ATOM	1104	C	LEU	A	819	32.445	4.699	77.808	1.00 26.91
ATOM	1105	O	LEU	A	819	32.394	5.907	77.557	1.00 20.81
ATOM	1106	CB	LEU	A	819	30.640	3.655	79.238	1.00 24.50
ATOM	1107	CG	LEU	A	819	29.199	3.116	79.294	1.00 23.57
ATOM	1108	CD1	LEU	A	819	28.780	2.812	80.728	1.00 22.54
ATOM	1109	CD2	LEU	A	819	28.256	4.174	78.693	1.00 27.51
ATOM	1124	N	LYS	A	822	33.403	5.748	74.210	1.00 22.26
ATOM	1125	CA	LYS	A	822	32.595	6.856	73.684	1.00 21.99
ATOM	1126	C	LYS	A	822	33.157	8.208	74.120	1.00 23.71
ATOM	1127	O	LYS	A	822	33.125	9.182	73.359	1.00 20.06
ATOM	1128	CB	LYS	A	822	31.123	6.713	74.115	1.00 24.02
ATOM	1129	CG	LYS	A	822	30.164	7.608	73.337	1.00 31.07
ATOM	1130	CD	LYS	A	822	28.727	7.077	73.410	1.00 38.28
ATOM	1131	CE	LYS	A	822	28.155	7.091	74.822	1.00 39.48
ATOM	1132	NZ	LYS	A	822	27.958	8.479	75.331	1.00 42.42

RARgamma Site II Residues (ref. 2LBD.pdb)

ATOM	110	N	SER	194	33.462	12.139	105.047	1.00 21.53
ATOM	111	CA	SER	194	32.239	12.265	104.247	1.00 21.04
ATOM	112	C	SER	194	31.924	13.712	103.899	1.00 21.80
ATOM	113	O	SER	194	31.727	14.047	102.732	1.00 21.17

ATOM	114	CB	SER	194	31.059	11.646	104.989	1.00	19.63
ATOM	115	OG	SER	194	29.904	11.654	104.183	1.00	19.69
ATOM	116	H	SER	194	33.433	11.608	105.870	1.00	13.44
ATOM	117	HG	SER	194	29.696	12.575	103.994	1.00	16.06
ATOM	118	N	LYS	195	31.894	14.557	104.925	1.00	22.99
ATOM	119	CA	LYS	195	31.614	15.981	104.797	1.00	22.87
ATOM	120	C	LYS	195	32.642	16.707	103.958	1.00	22.28
ATOM	121	O	LYS	195	32.278	17.511	103.124	1.00	23.38
ATOM	122	CB	LYS	195	31.496	16.626	106.180	1.00	23.64
ATOM	123	CG	LYS	195	30.078	16.572	106.747	1.00	28.29
ATOM	124	CD	LYS	195	29.209	15.582	105.952	1.00	30.25
ATOM	125	CE	LYS	195	27.736	15.623	106.362	1.00	32.32
ATOM	126	NZ	LYS	195	27.053	16.905	105.983	1.00	33.22
ATOM	127	H	LYS	195	32.099	14.210	105.821	1.00	12.80
ATOM	128	1HZ	LYS	195	27.088	17.060	104.958	1.00	15.82
ATOM	129	2HZ	LYS	195	26.063	16.878	106.305	1.00	15.26
ATOM	130	3HZ	LYS	195	27.530	17.695	106.469	1.00	11.80
ATOM	131	N	ALA	196	33.923	16.430	104.165	1.00	21.84
ATOM	132	CA	ALA	196	34.952	17.086	103.377	1.00	21.79
ATOM	133	C	ALA	196	34.725	16.717	101.913	1.00	21.34
ATOM	134	O	ALA	196	34.829	17.563	101.024	1.00	23.62
ATOM	135	CB	ALA	196	36.347	16.659	103.841	1.00	20.88
ATOM	136	H	ALA	196	34.178	15.781	104.855	1.00	21.01
ATOM	137	N	HIS	197	34.378	15.465	101.645	1.00	20.81
ATOM	138	CA	HIS	197	34.128	15.073	100.265	1.00	20.38
ATOM	139	C	HIS	197	32.896	15.796	99.701	1.00	21.21
ATOM	140	O	HIS	197	32.952	16.388	98.621	1.00	22.59
ATOM	141	CB	HIS	197	33.968	13.568	100.113	1.00	18.26
ATOM	142	CG	HIS	197	33.600	13.156	98.727	1.00	19.16
ATOM	143	ND1	HIS	197	34.524	13.060	97.706	1.00	19.65
ATOM	144	CD2	HIS	197	32.406	12.825	98.183	1.00	17.84
ATOM	145	CE1	HIS	197	33.917	12.682	96.598	1.00	18.43
ATOM	146	NE2	HIS	197	32.633	12.531	96.862	1.00	20.25
ATOM	147	H	HIS	197	34.300	14.821	102.382	1.00	16.92
ATOM	148	HD1	HIS	197	35.497	13.235	97.727	1.00	15.58
ATOM	149	HE2	HIS	197	31.936	12.266	96.223	1.00	12.28
ATOM	150	N	GLN	198	31.791	15.775	100.427	1.00	21.25
ATOM	151	CA	GLN	198	30.600	16.434	99.941	1.00	23.59
ATOM	152	C	GLN	198	30.828	17.916	99.658	1.00	24.07
ATOM	153	O	GLN	198	30.421	18.441	98.617	1.00	25.03

ATOM	154	CB	GLN	198	29.500	16.304	100.961	1.00	26.42
ATOM	155	CG	GLN	198	28.782	14.985	100.984	1.00	29.27
ATOM	156	CD	GLN	198	27.891	14.931	102.190	1.00	30.05
ATOM	157	OE1	GLN	198	27.411	15.972	102.653	1.00	31.98
ATOM	158	NE2	GLN	198	27.736	13.745	102.771	1.00	31.27
ATOM	159	H	GLN	198	31.789	15.330	101.298	1.00	16.00
ATOM	160	1HE2	GLN	198	27.144	13.729	103.551	1.00	15.85
ATOM	161	2HE2	GLN	198	28.203	12.971	102.398	1.00	16.16
ATOM	162	N	GLU	199	31.470	18.584	100.606	1.00	25.01
ATOM	163	CA	GLU	199	31.773	20.002	100.512	1.00	24.53
ATOM	164	C	GLU	199	32.720	20.377	99.400	1.00	23.37
ATOM	165	O	GLU	199	32.675	21.495	98.934	1.00	24.39
ATOM	166	CB	GLU	199	32.301	20.506	101.837	1.00	24.38
ATOM	167	CG	GLU	199	31.213	20.542	102.874	1.00	27.91
ATOM	168	CD	GLU	199	31.673	21.119	104.186	1.00	29.06
ATOM	169	OE1	GLU	199	32.496	22.065	104.169	1.00	30.26
ATOM	170	OE2	GLU	199	31.194	20.639	105.238	1.00	32.53
ATOM	171	H	GLU	199	31.753	18.106	101.411	1.00	12.27
ATOM	172	N	THR	200	33.561	19.449	98.960	1.00	21.99
ATOM	173	CA	THR	200	34.505	19.726	97.877	1.00	20.58
ATOM	174	C	THR	200	34.103	19.054	96.553	1.00	19.62
ATOM	175	O	THR	200	34.807	19.163	95.548	1.00	17.71
ATOM	176	CB	THR	200	35.934	19.275	98.260	1.00	20.42
ATOM	177	OG1	THR	200	36.007	17.835	98.247	1.00	17.20
ATOM	178	CG2	THR	200	36.299	19.831	99.658	1.00	18.24
ATOM	179	H	THR	200	33.574	18.555	99.363	1.00	15.26
ATOM	180	HG1	THR	200	35.526	17.536	99.027	1.00	18.31
ATOM	181	N	PHE	201	32.993	18.328	96.561	1.00	20.00
ATOM	182	CA	PHE	201	32.535	17.665	95.354	1.00	21.05
ATOM	183	C	PHE	201	31.047	17.393	95.340	1.00	21.47
ATOM	184	O	PHE	201	30.604	16.377	95.848	1.00	22.07
ATOM	185	CB	PHE	201	33.245	16.338	95.183	1.00	22.20
ATOM	186	CG	PHE	201	33.122	15.769	93.814	1.00	21.15
ATOM	187	CD1	PHE	201	33.696	16.424	92.727	1.00	24.07
ATOM	188	CD2	PHE	201	32.499	14.558	93.610	1.00	23.24
ATOM	189	CE1	PHE	201	33.660	15.871	91.458	1.00	23.53
ATOM	190	CE2	PHE	201	32.454	13.993	92.347	1.00	21.82
ATOM	191	CZ	PHE	201	33.041	14.655	91.268	1.00	22.68
ATOM	192	H	PHE	201	32.482	18.197	97.386	1.00	15.60
ATOM	193	N	PRO	202	30.269	18.256	94.680	1.00	23.56

ATOM	194	CA	PRO	202	28.812	18.163	94.548	1.00	23.81
ATOM	195	C	PRO	202	28.400	16.880	93.861	1.00	24.15
ATOM	196	O	PRO	202	29.039	16.462	92.888	1.00	23.02
ATOM	197	CB	PRO	202	28.485	19.348	93.655	1.00	23.88
ATOM	198	CG	PRO	202	29.475	20.339	94.055	1.00	25.50
ATOM	199	CD	PRO	202	30.750	19.528	94.119	1.00	24.92
ATOM	496	N	LEU	233	38.159	23.558	84.412	1.00	13.93
ATOM	497	CA	LEU	233	37.402	22.729	85.345	1.00	13.81
ATOM	498	C	LEU	233	38.315	21.721	86.032	1.00	13.48
ATOM	499	O	LEU	233	38.108	21.387	87.192	1.00	15.95
ATOM	500	CB	LEU	233	36.250	22.001	84.634	1.00	12.25
ATOM	501	CG	LEU	233	35.083	22.858	84.105	1.00	12.32
ATOM	502	CD1	LEU	233	34.147	21.981	83.337	1.00	12.38
ATOM	503	CD2	LEU	233	34.336	23.557	85.223	1.00	13.65
ATOM	504	H	LEU	233	37.941	23.494	83.454	1.00	14.66
ATOM	505	N	ALA	234	39.324	21.233	85.327	1.00	12.52
ATOM	506	CA	ALA	234	40.243	20.291	85.935	1.00	14.87
ATOM	507	C	ALA	234	41.085	21.048	86.995	1.00	16.06
ATOM	508	O	ALA	234	41.209	20.596	88.141	1.00	15.82
ATOM	509	CB	ALA	234	41.133	19.635	84.876	1.00	13.08
ATOM	510	H	ALA	234	39.421	21.484	84.388	1.00	18.02
ATOM	546	N	CYS	237	39.285	21.662	90.004	1.00	14.60
ATOM	547	CA	CYS	237	39.063	20.411	90.679	1.00	16.39
ATOM	548	C	CYS	237	40.287	20.070	91.534	1.00	16.47
ATOM	549	O	CYS	237	40.160	19.703	92.703	1.00	17.24
ATOM	550	CB	CYS	237	38.720	19.278	89.708	1.00	14.97
ATOM	551	SG	CYS	237	37.905	17.917	90.622	1.00	17.49
ATOM	552	H	CYS	237	39.424	21.679	89.042	1.00	13.36
ATOM	553	N	ILE	238	41.477	20.237	90.969	1.00	15.33
ATOM	554	CA	ILE	238	42.705	19.945	91.699	1.00	13.85
ATOM	555	C	ILE	238	42.774	20.741	93.007	1.00	14.22
ATOM	556	O	ILE	238	43.224	20.252	94.044	1.00	14.79
ATOM	557	CB	ILE	238	43.889	20.245	90.810	1.00	13.01
ATOM	558	CG1	ILE	238	43.899	19.259	89.634	1.00	12.70
ATOM	559	CG2	ILE	238	45.188	20.219	91.616	1.00	14.88
ATOM	560	CD1	ILE	238	44.860	19.636	88.559	1.00	10.75
ATOM	561	H	ILE	238	41.538	20.554	90.045	1.00	16.76
ATOM	562	N	ILE	239	42.358	21.990	92.940	1.00	14.17
ATOM	563	CA	ILE	239	42.329	22.858	94.107	1.00	14.19
ATOM	564	C	ILE	239	41.325	22.268	95.102	1.00	14.54

ATOM	565	O	ILE	239	41.582	22.238	96.299	1.00	14.16
ATOM	566	CB	ILE	239	41.910	24.293	93.703	1.00	14.59
ATOM	567	CG1	ILE	239	43.095	25.050	93.099	1.00	13.80
ATOM	568	CG2	ILE	239	41.339	25.024	94.871	1.00	15.96
ATOM	569	CD1	ILE	239	42.680	26.334	92.386	1.00	13.34
ATOM	570	H	ILE	239	42.056	22.353	92.079	1.00	18.53
ATOM	571	N	LYS	240	40.201	21.764	94.615	1.00	15.39
ATOM	572	CA	LYS	240	39.220	21.175	95.515	1.00	15.53
ATOM	573	C	LYS	240	39.718	19.879	96.140	1.00	15.65
ATOM	574	O	LYS	240	39.295	19.531	97.244	1.00	13.48
ATOM	575	CB	LYS	240	37.885	20.951	94.810	1.00	18.27
ATOM	576	CG	LYS	240	37.099	22.226	94.594	1.00	21.05
ATOM	577	CD	LYS	240	36.331	22.615	95.838	1.00	23.72
ATOM	578	CE	LYS	240	36.215	24.137	96.000	1.00	27.33
ATOM	579	NZ	LYS	240	37.448	24.762	96.648	1.00	30.09
ATOM	580	H	LYS	240	39.995	21.825	93.653	1.00	14.20
ATOM	581	1HZ	LYS	240	37.590	24.341	97.587	1.00	18.02
ATOM	582	2HZ	LYS	240	38.287	24.568	96.066	1.00	14.97
ATOM	583	3HZ	LYS	240	37.322	25.789	96.751	1.00	16.98
ATOM	584	N	ILE	241	40.619	19.179	95.447	1.00	14.37
ATOM	585	CA	ILE	241	41.183	17.934	95.962	1.00	15.71
ATOM	586	C	ILE	241	42.175	18.268	97.083	1.00	16.21
ATOM	587	O	ILE	241	42.213	17.598	98.123	1.00	15.85
ATOM	588	CB	ILE	241	41.852	17.092	94.849	1.00	15.46
ATOM	589	CG1	ILE	241	40.770	16.452	93.981	1.00	16.06
ATOM	590	CG2	ILE	241	42.699	15.981	95.448	1.00	17.68
ATOM	591	CD1	ILE	241	41.249	15.771	92.705	1.00	17.03
ATOM	592	H	ILE	241	40.882	19.507	94.561	1.00	16.01
ATOM	593	N	VAL	242	42.955	19.330	96.874	1.00	17.19
ATOM	594	CA	VAL	242	43.919	19.797	97.869	1.00	16.87
ATOM	595	C	VAL	242	43.155	20.219	99.116	1.00	16.56
ATOM	596	O	VAL	242	43.539	19.863	100.225	1.00	16.69
ATOM	597	CB	VAL	242	44.756	20.963	97.348	1.00	15.52
ATOM	598	CG1	VAL	242	45.481	21.614	98.481	1.00	15.69
ATOM	599	CG2	VAL	242	45.739	20.461	96.299	1.00	16.20
ATOM	600	H	VAL	242	42.885	19.801	96.014	1.00	17.48
ATOM	601	N	GLU	243	42.046	20.930	98.929	1.00	16.45
ATOM	602	CA	GLU	243	41.213	21.338	100.062	1.00	19.31
ATOM	603	C	GLU	243	40.680	20.112	100.818	1.00	17.64
ATOM	604	O	GLU	243	40.579	20.125	102.024	1.00	14.49

ATOM	605	CB	GLU	243	40.013	22.160	99.601	1.00	22.56
ATOM	606	CG	GLU	243	39.152	22.517	100.780	1.00	27.44
ATOM	607	CD	GLU	243	37.781	23.001	100.416	1.00	31.18
ATOM	608	OE1	GLU	243	37.679	23.810	99.463	1.00	33.07
ATOM	609	OE2	GLU	243	36.810	22.586	101.109	1.00	33.67
ATOM	610	H	GLU	243	41.792	21.201	98.022	1.00	15.45
ATOM	611	N	PHE	244	40.256	19.100	100.064	1.00	18.29
ATOM	612	CA	PHE	244	39.743	17.837	100.600	1.00	16.37
ATOM	613	C	PHE	244	40.842	17.147	101.406	1.00	15.24
ATOM	614	O	PHE	244	40.595	16.721	102.531	1.00	15.07
ATOM	615	CB	PHE	244	39.277	16.927	99.452	1.00	17.51
ATOM	616	CG	PHE	244	38.981	15.503	99.858	1.00	14.72
ATOM	617	CD1	PHE	244	37.831	15.187	100.549	1.00	15.04
ATOM	618	CD2	PHE	244	39.845	14.479	99.500	1.00	15.96
ATOM	619	CE1	PHE	244	37.540	13.862	100.880	1.00	16.72
ATOM	620	CE2	PHE	244	39.565	13.154	99.823	1.00	16.27
ATOM	621	CZ	PHE	244	38.405	12.845	100.518	1.00	14.78
ATOM	622	H	PHE	244	40.258	19.205	99.089	1.00	13.23
ATOM	814	N	ALA	266	48.576	10.971	93.812	1.00	15.90
ATOM	815	CA	ALA	266	47.182	10.496	93.792	1.00	17.39
ATOM	816	C	ALA	266	46.167	11.428	93.127	1.00	17.22
ATOM	817	O	ALA	266	45.012	11.043	92.903	1.00	16.41
ATOM	818	CB	ALA	266	46.722	10.185	95.222	1.00	16.38
ATOM	819	H	ALA	266	48.811	11.745	94.370	1.00	15.48
ATOM	820	N	CYS	267	46.597	12.643	92.802	1.00	15.91
ATOM	821	CA	CYS	267	45.700	13.622	92.214	1.00	17.69
ATOM	822	C	CYS	267	44.940	13.171	90.958	1.00	16.15
ATOM	823	O	CYS	267	43.718	13.343	90.888	1.00	14.43
ATOM	824	CB	CYS	267	46.438	14.920	91.951	1.00	18.90
ATOM	825	SG	CYS	267	45.310	16.241	91.678	1.00	23.66
ATOM	826	H	CYS	267	47.530	12.902	92.957	1.00	11.70
ATOM	827	N	LEU	268	45.650	12.573	89.999	1.00	14.38
ATOM	828	CA	LEU	268	45.009	12.091	88.787	1.00	15.09
ATOM	829	C	LEU	268	44.049	10.961	89.129	1.00	15.22
ATOM	830	O	LEU	268	42.932	10.926	88.602	1.00	15.41
ATOM	831	CB	LEU	268	46.037	11.609	87.758	1.00	14.82
ATOM	832	CG	LEU	268	45.922	12.104	86.291	1.00	16.13
ATOM	833	CD1	LEU	268	46.809	11.216	85.363	1.00	13.28
ATOM	834	CD2	LEU	268	44.465	12.106	85.808	1.00	13.62
ATOM	835	H	LEU	268	46.624	12.472	90.107	1.00	11.61

ATOM	836	N	ASP	269	44.475	10.032	89.989	1.00	14.39
ATOM	837	CA	ASP	269	43.610	8.927	90.390	1.00	14.73
ATOM	838	C	ASP	269	42.264	9.494	90.826	1.00	16.42
ATOM	839	O	ASP	269	41.214	9.159	90.250	1.00	17.01
ATOM	840	CB	ASP	269	44.193	8.164	91.583	1.00	16.26
ATOM	841	CG	ASP	269	45.461	7.396	91.251	1.00	16.52
ATOM	842	OD1	ASP	269	46.050	7.627	90.207	1.00	18.78
ATOM	843	OD2	ASP	269	45.887	6.548	92.057	1.00	19.84
ATOM	844	H	ASP	269	45.390	10.079	90.347	1.00	13.22
ATOM	845	N	ILE	270	42.299	10.400	91.809	1.00	16.86
ATOM	846	CA	ILE	270	41.069	10.996	92.356	1.00	16.75
ATOM	847	C	ILE	270	40.260	11.805	91.336	1.00	15.88
ATOM	848	O	ILE	270	39.035	11.758	91.345	1.00	16.48
ATOM	849	CB	ILE	270	41.351	11.838	93.625	1.00	16.55
ATOM	850	CG1	ILE	270	42.034	10.972	94.680	1.00	15.45
ATOM	851	CG2	ILE	270	40.046	12.388	94.221	1.00	16.85
ATOM	852	CD1	ILE	270	42.364	11.741	95.933	1.00	18.34
ATOM	853	H	ILE	270	43.171	10.675	92.167	1.00	13.31
ATOM	854	N	LEU	271	40.932	12.535	90.458	1.00	15.65
ATOM	855	CA	LEU	271	40.246	13.308	89.430	1.00	16.49
ATOM	856	C	LEU	271	39.456	12.294	88.580	1.00	16.41
ATOM	857	O	LEU	271	38.294	12.530	88.244	1.00	17.42
ATOM	858	CB	LEU	271	41.297	14.038	88.597	1.00	16.24
ATOM	859	CG	LEU	271	41.309	15.557	88.415	1.00	17.43
ATOM	860	CD1	LEU	271	40.654	16.308	89.533	1.00	14.58
ATOM	861	CD2	LEU	271	42.735	16.005	88.203	1.00	16.24
ATOM	862	H	LEU	271	41.910	12.566	90.512	1.00	15.08
ATOM	863	N	MET	272	40.060	11.131	88.316	1.00	16.60
ATOM	864	CA	MET	272	39.418	10.073	87.528	1.00	16.79
ATOM	865	C	MET	272	38.250	9.441	88.300	1.00	17.44
ATOM	866	O	MET	272	37.176	9.161	87.733	1.00	19.90
ATOM	867	CB	MET	272	40.420	8.978	87.127	1.00	17.65
ATOM	868	CG	MET	272	41.448	9.392	86.102	1.00	18.79
ATOM	869	SD	MET	272	40.799	9.486	84.419	1.00	22.97
ATOM	870	CE	MET	272	42.292	9.289	83.461	1.00	19.64
ATOM	871	H	MET	272	40.964	10.976	88.662	1.00	18.75
ATOM	872	N	LEU	273	38.441	9.179	89.581	1.00	14.90
ATOM	873	CA	LEU	273	37.356	8.606	90.339	1.00	14.87
ATOM	874	C	LEU	273	36.185	9.588	90.339	1.00	15.34
ATOM	875	O	LEU	273	35.037	9.194	90.129	1.00	15.36

ATOM	876	CB	LEU	273	37.809	8.343	91.761	1.00	15.48
ATOM	877	CG	LEU	273	36.730	7.760	92.651	1.00	16.54
ATOM	878	CD1	LEU	273	36.312	6.404	92.086	1.00	17.29
ATOM	879	CD2	LEU	273	37.282	7.620	94.064	1.00	15.37
ATOM	880	H	LEU	273	39.308	9.367	89.992	1.00	16.64
ATOM	881	N	ARG	274	36.494	10.873	90.528	1.00	15.34
ATOM	882	CA	ARG	274	35.486	11.919	90.572	1.00	15.78
ATOM	883	C	ARG	274	34.629	12.006	89.328	1.00	17.06
ATOM	884	O	ARG	274	33.434	11.812	89.437	1.00	18.66
ATOM	885	CB	ARG	274	36.095	13.267	90.936	1.00	16.75
ATOM	886	CG	ARG	274	36.461	13.333	92.429	1.00	17.30
ATOM	887	CD	ARG	274	36.835	14.716	92.892	1.00	17.86
ATOM	888	NE	ARG	274	36.951	14.740	94.351	1.00	21.93
ATOM	889	CZ	ARG	274	37.027	15.844	95.093	1.00	22.23
ATOM	890	NH1	ARG	274	36.998	17.045	94.520	1.00	21.99
ATOM	891	NH2	ARG	274	37.115	15.745	96.413	1.00	20.01
ATOM	892	H	ARG	274	37.434	11.117	90.631	1.00	16.07
ATOM	893	HE	ARG	274	36.978	13.875	94.802	1.00	14.88
ATOM	894	1HH1	ARG	274	36.923	17.134	93.527	1.00	14.06
ATOM	895	2HH1	ARG	274	37.061	17.866	95.089	1.00	14.03
ATOM	896	1HH2	ARG	274	37.122	14.847	96.850	1.00	17.31
ATOM	897	2HH2	ARG	274	37.173	16.572	96.971	1.00	14.92
ATOM	914	N	THR	277	32.271	9.023	88.779	1.00	13.95
ATOM	915	CA	THR	277	31.115	8.905	89.661	1.00	15.92
ATOM	916	C	THR	277	30.004	9.856	89.186	1.00	17.31
ATOM	917	O	THR	277	28.859	9.761	89.626	1.00	19.20
ATOM	918	CB	THR	277	31.471	9.205	91.138	1.00	18.17
ATOM	919	OG1	THR	277	31.879	10.567	91.267	1.00	20.50
ATOM	920	CG2	THR	277	32.613	8.315	91.605	1.00	19.00
ATOM	921	H	THR	277	33.002	9.624	89.038	1.00	16.11
ATOM	922	HG1	THR	277	32.699	10.722	90.788	1.00	14.03
ATOM	923	N	ARG	278	30.352	10.756	88.266	1.00	17.51
ATOM	924	CA	ARG	278	29.428	11.741	87.669	1.00	17.48
ATOM	925	C	ARG	278	28.907	11.260	86.280	1.00	16.92
ATOM	926	O	ARG	278	28.552	12.046	85.396	1.00	16.64
ATOM	927	CB	ARG	278	30.176	13.060	87.508	1.00	17.18
ATOM	928	CG	ARG	278	30.446	13.774	88.808	1.00	16.64
ATOM	929	CD	ARG	278	29.338	14.762	89.057	1.00	17.73
ATOM	930	NE	ARG	278	29.640	15.725	90.108	1.00	17.21
ATOM	931	CZ	ARG	278	30.658	16.570	90.085	1.00	19.13

ATOM	932	NH1	ARG	278	31.499	16.576	89.060	1.00	20.62
ATOM	933	NH2	ARG	278	30.816	17.433	91.081	1.00	20.16
ATOM	934	H	ARG	278	31.277	10.787	87.949	1.00	13.43
ATOM	935	HE	ARG	278	29.047	15.731	90.894	1.00	15.33
ATOM	936	1HH1	ARG	278	31.378	15.948	88.280	1.00	16.80
ATOM	937	2HH1	ARG	278	32.325	17.162	89.023	1.00	14.95
ATOM	938	1HH2	ARG	278	30.169	17.426	91.850	1.00	14.24
ATOM	939	2HH2	ARG	278	31.583	18.098	91.094	1.00	15.16
ATOM	954	N	THR	280	26.282	9.265	83.776	1.00	17.68
ATOM	955	CA	THR	280	24.869	8.925	83.581	1.00	18.60
ATOM	956	C	THR	280	24.815	7.906	82.476	1.00	18.63
ATOM	957	O	THR	280	25.028	8.237	81.316	1.00	19.24
ATOM	958	CB	THR	280	24.038	10.130	83.148	1.00	18.35
ATOM	959	OG1	THR	280	24.226	11.205	84.076	1.00	19.23
ATOM	960	CG2	THR	280	22.590	9.770	83.156	1.00	19.36
ATOM	961	H	THR	280	26.736	9.748	83.057	1.00	16.32
ATOM	962	HG1	THR	280	25.144	11.476	84.000	1.00	9.92
ATOM	963	N	PRO	281	24.538	6.648	82.822	1.00	19.26
ATOM	964	CA	PRO	281	24.470	5.596	81.828	1.00	23.13
ATOM	965	C	PRO	281	23.422	5.934	80.771	1.00	27.05
ATOM	966	O	PRO	281	23.723	5.886	79.589	1.00	29.83
ATOM	967	CB	PRO	281	24.055	4.378	82.659	1.00	21.19
ATOM	968	CG	PRO	281	24.526	4.683	83.975	1.00	19.03
ATOM	969	CD	PRO	281	24.140	6.111	84.126	1.00	19.67
ATOM	970	N	GLU	282	22.225	6.347	81.201	1.00	29.52
ATOM	971	CA	GLU	282	21.114	6.686	80.289	1.00	30.92
ATOM	972	C	GLU	282	21.496	7.566	79.079	1.00	29.16
ATOM	973	O	GLU	282	21.189	7.244	77.923	1.00	29.44
ATOM	974	CB	GLU	282	19.949	7.342	81.083	1.00	34.18
ATOM	975	CG	GLU	282	18.596	6.561	81.059	1.00	37.63
ATOM	976	CD	GLU	282	17.598	7.038	79.975	1.00	39.35
ATOM	977	OE1	GLU	282	17.763	6.709	78.769	1.00	39.81
ATOM	978	OE2	GLU	282	16.628	7.737	80.345	1.00	40.91
ATOM	979	H	GLU	282	22.043	6.390	82.163	1.00	14.17
ATOM	1048	N	ASP	290	30.544	22.243	87.680	1.00	18.56
ATOM	1049	CA	ASP	290	29.751	23.433	87.443	1.00	16.64
ATOM	1050	C	ASP	290	28.396	23.055	86.781	1.00	16.67
ATOM	1051	O	ASP	290	27.492	23.889	86.648	1.00	16.11
ATOM	1052	CB	ASP	290	30.547	24.465	86.627	1.00	19.14
ATOM	1053	CG	ASP	290	30.679	24.105	85.162	1.00	17.90

ATOM	1054	OD1	ASP	290	30.715	22.918	84.812	1.00	19.78
ATOM	1055	OD2	ASP	290	30.765	25.038	84.360	1.00	17.99
ATOM	1056	H	ASP	290	31.098	21.861	86.974	1.00	13.42
ATOM	1393	N	THR	328	32.657	6.889	98.484	1.00	12.39
ATOM	1394	CA	THR	328	33.499	7.531	97.480	1.00	14.32
ATOM	1395	C	THR	328	34.507	8.459	98.191	1.00	13.38
ATOM	1396	O	THR	328	35.684	8.521	97.820	1.00	12.40
ATOM	1397	CB	THR	328	32.650	8.351	96.491	1.00	12.84
ATOM	1398	OG1	THR	328	31.708	7.492	95.841	1.00	14.19
ATOM	1399	CG2	THR	328	33.517	8.994	95.486	1.00	12.73
ATOM	1400	H	THR	328	31.697	7.093	98.476	1.00	17.66
ATOM	1401	HG1	THR	328	32.184	6.794	95.373	1.00	15.73
ATOM	1402	N	GLY	329	34.037	9.169	99.218	1.00	14.14
ATOM	1403	CA	GLY	329	34.898	10.063	99.963	1.00	10.87
ATOM	1404	C	GLY	329	35.973	9.248	100.634	1.00	11.08
ATOM	1405	O	GLY	329	37.146	9.586	100.525	1.00	11.93
ATOM	1406	H	GLY	329	33.106	9.075	99.503	1.00	18.91
ATOM	1425	N	SER	332	38.488	7.748	98.210	1.00	12.43
ATOM	1426	CA	SER	332	39.440	8.792	97.800	1.00	12.96
ATOM	1427	C	SER	332	40.505	9.050	98.856	1.00	12.57
ATOM	1428	O	SER	332	41.677	9.204	98.527	1.00	11.85
ATOM	1429	CB	SER	332	38.720	10.109	97.515	1.00	12.28
ATOM	1430	OG	SER	332	37.815	9.953	96.454	1.00	15.83
ATOM	1431	H	SER	332	37.552	7.988	98.365	1.00	18.36
ATOM	1432	HG	SER	332	37.203	9.240	96.682	1.00	17.36

RXRalpha Site II Residues (ref. 1LBD.pdb)

ATOM	87	N	LEU	236	30.657	84.317	63.377	1.00	35.43
ATOM	88	CA	LEU	236	29.844	85.467	63.046	1.00	35.76
ATOM	89	C	LEU	236	29.344	85.142	61.634	1.00	36.91
ATOM	90	O	LEU	236	28.157	85.245	61.327	1.00	37.85
ATOM	91	CB	LEU	236	30.713	86.718	62.998	1.00	34.14
ATOM	92	CG	LEU	236	30.091	88.105	63.184	1.00	35.41
ATOM	93	CD1	LEU	236	31.028	89.058	62.487	1.00	38.27
ATOM	94	CD2	LEU	236	28.654	88.262	62.637	1.00	36.08
ATOM	95	N	GLU	237	30.280	84.697	60.804	1.00	37.85
ATOM	96	CA	GLU	237	30.055	84.311	59.414	1.00	37.03
ATOM	97	C	GLU	237	28.875	83.317	59.253	1.00	36.46

ATOM	98	O	GLU	237	27.977	83.527	58.431	1.00	33.55
ATOM	99	CB	GLU	237	31.365	83.701	58.898	1.00	39.91
ATOM	100	CG	GLU	237	31.585	83.796	57.431	1.00	42.42
ATOM	101	CD	GLU	237	30.519	83.050	56.702	1.00	49.05
ATOM	102	OE1	GLU	237	30.598	81.800	56.680	1.00	52.01
ATOM	103	OE2	GLU	237	29.567	83.707	56.208	1.00	53.07
ATOM	104	N	ALA	238	28.854	82.285	60.096	1.00	39.98
ATOM	105	CA	ALA	238	27.821	81.232	60.093	1.00	37.99
ATOM	106	C	ALA	238	26.415	81.715	60.408	1.00	35.29
ATOM	107	O	ALA	238	25.458	81.248	59.801	1.00	34.55
ATOM	108	CB	ALA	238	28.221	80.063	61.066	1.00	33.06
ATOM	109	N	GLU	239	26.286	82.615	61.380	1.00	35.97
ATOM	110	CA	GLU	239	24.967	83.135	61.755	1.00	38.46
ATOM	111	C	GLU	239	24.490	83.961	60.599	1.00	39.38
ATOM	112	O	GLU	239	23.401	83.752	60.096	1.00	42.38
ATOM	113	CB	GLU	239	25.002	84.017	63.031	1.00	38.94
ATOM	114	CG	GLU	239	25.017	83.277	64.403	1.00	37.77
ATOM	115	CD	GLU	239	23.716	82.538	64.709	1.00	34.29
ATOM	116	OE1	GLU	239	22.637	83.173	64.751	1.00	34.87
ATOM	117	OE2	GLU	239	23.777	81.307	64.903	1.00	28.74
ATOM	118	N	LEU	240	25.342	84.884	60.164	1.00	40.88
ATOM	119	CA	LEU	240	25.042	85.771	59.043	1.00	36.87
ATOM	120	C	LEU	240	24.747	84.943	57.829	1.00	35.24
ATOM	121	O	LEU	240	23.789	85.202	57.109	1.00	34.29
ATOM	122	CB	LEU	240	26.201	86.733	58.777	1.00	34.15
ATOM	123	CG	LEU	240	26.032	87.969	59.663	1.00	36.58
ATOM	124	CD1	LEU	240	27.280	88.842	59.591	1.00	40.07
ATOM	125	CD2	LEU	240	24.745	88.728	59.280	1.00	32.86
ATOM	126	N	ALA	241	25.492	83.868	57.668	1.00	33.12
ATOM	127	CA	ALA	241	25.266	82.987	56.544	1.00	32.07
ATOM	128	C	ALA	241	23.882	82.367	56.562	1.00	28.57
ATOM	129	O	ALA	241	23.554	81.610	55.664	1.00	30.72
ATOM	130	CB	ALA	241	26.291	81.900	56.537	1.00	34.96
ATOM	131	N	VAL	242	23.051	82.725	57.533	1.00	28.22
ATOM	132	CA	VAL	242	21.738	82.120	57.636	1.00	25.21
ATOM	133	C	VAL	242	20.623	83.069	58.183	1.00	25.77
ATOM	134	O	VAL	242	19.550	82.653	58.631	1.00	23.41
ATOM	135	CB	VAL	242	21.899	80.842	58.444	1.00	22.99
ATOM	136	CG1	VAL	242	21.975	81.138	59.916	1.00	21.73
ATOM	137	CG2	VAL	242	20.846	79.898	58.098	1.00	23.34

ATOM	138	N	GLU	243	20.873	84.366	58.050	1.00	29.04
ATOM	139	CA	GLU	243	19.955	85.420	58.485	1.00	31.55
ATOM	140	C	GLU	243	18.790	85.495	57.515	1.00	32.99
ATOM	141	O	GLU	243	19.016	85.500	56.315	1.00	36.40
ATOM	142	CB	GLU	243	20.697	86.738	58.401	1.00	33.53
ATOM	143	CG	GLU	243	19.950	87.907	58.936	1.00	38.25
ATOM	144	CD	GLU	243	20.565	88.357	60.224	1.00	42.27
ATOM	145	OE1	GLU	243	21.818	88.544	60.242	1.00	36.36
ATOM	146	OE2	GLU	243	19.800	88.483	61.221	1.00	49.21
ATOM	147	N	PRO	244	17.555	85.687	58.001	1.00	33.30
ATOM	148	CA	PRO	244	16.452	85.759	57.055	1.00	36.93
ATOM	149	C	PRO	244	16.587	87.115	56.376	1.00	42.25
ATOM	150	O	PRO	244	16.983	88.088	57.009	1.00	44.70
ATOM	151	CB	PRO	244	15.215	85.718	57.947	1.00	39.57
ATOM	152	CG	PRO	244	15.726	85.581	59.340	1.00	35.65
ATOM	153	CD	PRO	244	17.100	86.165	59.302	1.00	36.07
ATOM	349	N	ALA	271	7.191	76.115	57.199	1.00	29.50
ATOM	350	CA	ALA	271	7.966	76.681	58.300	1.00	27.28
ATOM	351	C	ALA	271	8.794	75.692	59.151	1.00	26.76
ATOM	352	O	ALA	271	9.872	76.064	59.652	1.00	27.26
ATOM	353	CB	ALA	271	7.083	77.497	59.168	1.00	23.29
ATOM	354	N	ALA	272	8.287	74.476	59.382	1.00	27.64
ATOM	355	CA	ALA	272	9.036	73.462	60.144	1.00	26.95
ATOM	356	C	ALA	272	10.327	73.296	59.374	1.00	29.21
ATOM	357	O	ALA	272	11.440	73.568	59.824	1.00	30.82
ATOM	358	CB	ALA	272	8.287	72.166	60.096	1.00	24.06
ATOM	376	N	GLN	275	12.864	76.169	59.278	1.00	28.33
ATOM	377	CA	GLN	275	13.609	76.269	60.539	1.00	26.75
ATOM	378	C	GLN	275	14.692	75.203	60.489	1.00	29.14
ATOM	379	O	GLN	275	15.879	75.506	60.635	1.00	30.79
ATOM	380	CB	GLN	275	12.723	76.046	61.766	1.00	20.91
ATOM	381	CG	GLN	275	11.564	76.979	61.849	1.00	21.96
ATOM	382	CD	GLN	275	10.817	76.871	63.163	1.00	22.43
ATOM	383	OE1	GLN	275	10.539	75.781	63.664	1.00	24.91
ATOM	384	NE2	GLN	275	10.445	78.011	63.705	1.00	20.62
ATOM	385	N	LEU	276	14.304	73.979	60.158	1.00	28.84
ATOM	386	CA	LEU	276	15.288	72.913	60.115	1.00	32.72
ATOM	387	C	LEU	276	16.523	73.357	59.349	1.00	33.75
ATOM	388	O	LEU	276	17.640	73.252	59.856	1.00	33.64
ATOM	389	CB	LEU	276	14.702	71.633	59.489	1.00	33.19

ATOM	390	CG	LEU	276	15.702	70.508	59.214	1.00	32.49
ATOM	391	CD1	LEU	276	16.333	70.081	60.488	1.00	30.89
ATOM	392	CD2	LEU	276	15.037	69.353	58.554	1.00	33.68
ATOM	393	N	PHE	277	16.320	73.920	58.158	1.00	32.96
ATOM	394	CA	PHE	277	17.466	74.336	57.359	1.00	33.52
ATOM	395	C	PHE	277	18.235	75.463	57.943	1.00	32.72
ATOM	396	O	PHE	277	19.473	75.425	57.951	1.00	34.61
ATOM	397	CB	PHE	277	17.148	74.608	55.892	1.00	38.91
ATOM	398	CG	PHE	277	17.934	73.734	54.955	1.00	46.04
ATOM	399	CD1	PHE	277	18.866	72.821	55.465	1.00	49.86
ATOM	400	CD2	PHE	277	17.733	73.786	53.588	1.00	46.15
ATOM	401	CE1	PHE	277	19.584	71.970	54.633	1.00	48.96
ATOM	402	CE2	PHE	277	18.450	72.931	52.738	1.00	51.33
ATOM	403	CZ	PHE	277	19.383	72.017	53.277	1.00	51.91
ATOM	404	N	THR	278	17.537	76.410	58.546	1.00	30.83
ATOM	405	CA	THR	278	18.263	77.507	59.141	1.00	29.49
ATOM	406	C	THR	278	19.159	76.951	60.228	1.00	30.33
ATOM	407	O	THR	278	20.045	77.647	60.721	1.00	32.94
ATOM	408	CB	THR	278	17.315	78.536	59.675	1.00	27.12
ATOM	409	OG1	THR	278	16.012	78.272	59.136	1.00	30.31
ATOM	410	CG2	THR	278	17.732	79.913	59.181	1.00	25.40
ATOM	411	N	LEU	279	18.987	75.647	60.491	1.00	29.99
ATOM	412	CA	LEU	279	19.702	74.886	61.510	1.00	31.31
ATOM	413	C	LEU	279	20.905	74.100	61.030	1.00	33.54
ATOM	414	O	LEU	279	22.025	74.363	61.505	1.00	38.01
ATOM	415	CB	LEU	279	18.734	73.930	62.206	1.00	33.42
ATOM	416	CG	LEU	279	18.683	73.794	63.722	1.00	28.79
ATOM	417	CD1	LEU	279	18.067	75.049	64.376	1.00	23.73
ATOM	418	CD2	LEU	279	17.859	72.574	63.990	1.00	27.75
ATOM	419	N	VAL	280	20.720	73.111	60.146	1.00	32.77
ATOM	420	CA	VAL	280	21.916	72.371	59.693	1.00	34.18
ATOM	421	C	VAL	280	22.902	73.298	58.968	1.00	34.17
ATOM	422	O	VAL	280	24.092	73.324	59.278	1.00	33.48
ATOM	423	CB	VAL	280	21.627	71.065	58.868	1.00	30.97
ATOM	424	CG1	VAL	280	20.352	70.358	59.369	1.00	31.67
ATOM	425	CG2	VAL	280	21.619	71.325	57.402	1.00	33.04
ATOM	426	N	GLU	281	22.383	74.162	58.109	1.00	31.06
ATOM	427	CA	GLU	281	23.273	75.071	57.406	1.00	31.66
ATOM	428	C	GLU	281	24.099	75.925	58.364	1.00	30.93
ATOM	429	O	GLU	281	25.203	76.339	58.016	1.00	31.16

ATOM	430	CB	GLU	281	22.536	75.961	56.385	1.00	35.28
ATOM	431	CG	GLU	281	21.923	75.246	55.168	1.00	34.78
ATOM	432	CD	GLU	281	22.864	74.267	54.486	1.00	32.73
ATOM	433	OE1	GLU	281	24.087	74.529	54.427	1.00	19.72
ATOM	434	OE2	GLU	281	22.351	73.222	54.004	1.00	32.69
ATOM	435	N	TRP	282	23.577	76.199	59.553	1.00	28.28
ATOM	436	CA	TRP	282	24.341	77.002	60.510	1.00	30.40
ATOM	437	C	TRP	282	25.429	76.091	61.158	1.00	35.40
ATOM	438	O	TRP	282	26.597	76.495	61.323	1.00	36.16
ATOM	439	CB	TRP	282	23.394	77.659	61.559	1.00	24.73
ATOM	440	CG	TRP	282	24.075	78.176	62.841	1.00	20.02
ATOM	441	CD1	TRP	282	24.751	79.359	63.006	1.00	19.84
ATOM	442	CD2	TRP	282	24.284	77.437	64.046	1.00	23.23
ATOM	443	NE1	TRP	282	25.410	79.380	64.213	1.00	16.40
ATOM	444	CE2	TRP	282	25.144	78.213	64.873	1.00	21.68
ATOM	445	CE3	TRP	282	23.843	76.185	64.507	1.00	20.19
ATOM	446	CZ2	TRP	282	25.579	77.772	66.120	1.00	19.31
ATOM	447	CZ3	TRP	282	24.275	75.748	65.747	1.00	22.95
ATOM	448	CH2	TRP	282	25.136	76.536	66.541	1.00	20.41
ATOM	620	N	GLY	304	20.287	69.044	70.953	1.00	29.43
ATOM	621	CA	GLY	304	20.094	70.450	71.256	1.00	29.15
ATOM	622	C	GLY	304	19.355	71.333	70.270	1.00	25.88
ATOM	623	O	GLY	304	19.573	72.527	70.332	1.00	29.72
ATOM	624	N	TRP	305	18.476	70.792	69.417	1.00	25.81
ATOM	625	CA	TRP	305	17.688	71.571	68.426	1.00	28.27
ATOM	626	C	TRP	305	16.862	72.793	68.914	1.00	31.21
ATOM	627	O	TRP	305	16.762	73.828	68.242	1.00	30.23
ATOM	628	CB	TRP	305	16.704	70.630	67.708	1.00	26.86
ATOM	629	CG	TRP	305	15.237	71.110	67.705	1.00	33.15
ATOM	630	CD1	TRP	305	14.740	72.346	67.290	1.00	36.35
ATOM	631	CD2	TRP	305	14.116	70.409	68.228	1.00	34.91
ATOM	632	NE1	TRP	305	13.396	72.446	67.562	1.00	32.18
ATOM	633	CE2	TRP	305	12.985	71.278	68.123	1.00	33.00
ATOM	634	CE3	TRP	305	13.960	69.140	68.776	1.00	32.73
ATOM	635	CZ2	TRP	305	11.732	70.909	68.545	1.00	33.45
ATOM	636	CZ3	TRP	305	12.711	68.776	69.195	1.00	42.77
ATOM	637	CH2	TRP	305	11.603	69.659	69.078	1.00	43.63
ATOM	638	N	ASN	306	16.035	72.530	69.918	1.00	33.01
ATOM	639	CA	ASN	306	15.130	73.503	70.502	1.00	33.62
ATOM	640	C	ASN	306	15.843	74.691	71.167	1.00	34.24

ATOM	641	O	ASN	306	15.381	75.822	71.143	1.00	35.65
ATOM	642	CB	ASN	306	14.244	72.755	71.505	1.00	35.17
ATOM	643	CG	ASN	306	15.028	72.250	72.740	1.00	39.33
ATOM	644	OD1	ASN	306	16.144	71.695	72.626	1.00	33.48
ATOM	645	ND2	ASN	306	14.441	72.464	73.939	1.00	39.83
ATOM	646	N	GLU	307	16.957	74.436	71.809	1.00	28.91
ATOM	647	CA	GLU	307	17.662	75.516	72.434	1.00	24.93
ATOM	648	C	GLU	307	18.318	76.379	71.384	1.00	22.24
ATOM	649	O	GLU	307	18.376	77.581	71.551	1.00	19.58
ATOM	650	CB	GLU	307	18.696	74.946	73.399	1.00	30.44
ATOM	651	CG	GLU	307	18.149	74.781	74.809	1.00	29.85
ATOM	652	CD	GLU	307	19.079	74.010	75.689	1.00	28.89
ATOM	653	OE1	GLU	307	19.983	74.601	76.331	1.00	28.55
ATOM	654	OE2	GLU	307	18.876	72.790	75.745	1.00	35.64
ATOM	655	N	LEU	308	18.814	75.758	70.306	1.00	24.10
ATOM	656	CA	LEU	308	19.482	76.450	69.185	1.00	23.45
ATOM	657	C	LEU	308	18.415	77.274	68.460	1.00	22.44
ATOM	658	O	LEU	308	18.652	78.424	68.085	1.00	24.47
ATOM	659	CB	LEU	308	20.165	75.436	68.228	1.00	19.67
ATOM	660	CG	LEU	308	21.367	74.560	68.688	1.00	19.56
ATOM	661	CD1	LEU	308	21.596	73.356	67.810	1.00	9.80
ATOM	662	CD2	LEU	308	22.642	75.355	68.781	1.00	18.92
ATOM	663	N	LEU	309	17.217	76.702	68.360	1.00	23.04
ATOM	664	CA	LEU	309	16.031	77.317	67.740	1.00	22.80
ATOM	665	C	LEU	309	15.537	78.579	68.499	1.00	28.05
ATOM	666	O	LEU	309	15.164	79.590	67.894	1.00	28.58
ATOM	667	CB	LEU	309	14.937	76.271	67.725	1.00	22.01
ATOM	668	CG	LEU	309	14.086	76.188	66.490	1.00	23.94
ATOM	669	CD1	LEU	309	13.043	77.266	66.523	1.00	27.11
ATOM	670	CD2	LEU	309	14.986	76.295	65.297	1.00	30.77
ATOM	671	N	ILE	310	15.543	78.503	69.833	1.00	32.40
ATOM	672	CA	ILE	310	15.141	79.589	70.745	1.00	28.14
ATOM	673	C	ILE	310	16.216	80.687	70.789	1.00	26.11
ATOM	674	O	ILE	310	15.914	81.862	70.668	1.00	23.24
ATOM	675	CB	ILE	310	14.926	79.021	72.201	1.00	31.03
ATOM	676	CG1	ILE	310	13.656	78.177	72.263	1.00	26.74
ATOM	677	CG2	ILE	310	14.828	80.140	73.253	1.00	34.33
ATOM	678	CD1	ILE	310	13.456	77.576	73.588	1.00	25.96
ATOM	679	N	ALA	311	17.474	80.291	70.942	1.00	27.15
ATOM	680	CA	ALA	311	18.563	81.255	71.023	1.00	28.97

ATOM	681	C	ALA	311	18.447	82.140	69.833	1.00	30.48
ATOM	682	O	ALA	311	18.723	83.330	69.917	1.00	36.17
ATOM	683	CB	ALA	311	19.899	80.565	71.033	1.00	29.09
ATOM	684	N	SER	312	17.968	81.554	68.736	1.00	30.86
ATOM	685	CA	SER	312	17.777	82.279	67.494	1.00	29.77
ATOM	686	C	SER	312	16.489	83.060	67.431	1.00	28.46
ATOM	687	O	SER	312	16.566	84.285	67.376	1.00	26.28
ATOM	688	CB	SER	312	17.900	81.363	66.288	1.00	32.52
ATOM	689	OG	SER	312	18.879	81.890	65.410	1.00	38.04
ATOM	707	N	HIS	315	16.912	86.232	69.632	1.00	31.29
ATOM	708	CA	HIS	315	17.794	87.294	69.157	1.00	29.26
ATOM	709	C	HIS	315	17.124	88.248	68.188	1.00	28.74
ATOM	710	O	HIS	315	16.855	89.395	68.551	1.00	27.46
ATOM	711	CB	HIS	315	19.072	86.763	68.525	1.00	31.22
ATOM	712	CG	HIS	315	20.217	87.709	68.665	1.00	31.31
ATOM	713	ND1	HIS	315	20.069	88.950	69.246	1.00	32.38
ATOM	714	CD2	HIS	315	21.536	87.565	68.422	1.00	32.42
ATOM	715	CE1	HIS	315	21.252	89.524	69.371	1.00	30.07
ATOM	716	NE2	HIS	315	22.161	88.704	68.878	1.00	33.09
ATOM	717	N	ARG	316	16.783	87.749	67.000	1.00	27.07
ATOM	718	CA	ARG	316	16.130	88.551	65.979	1.00	29.67
ATOM	719	C	ARG	316	14.912	89.275	66.509	1.00	29.29
ATOM	720	O	ARG	316	14.552	90.351	66.018	1.00	34.98
ATOM	721	CB	ARG	316	15.779	87.678	64.783	1.00	31.58
ATOM	722	CG	ARG	316	14.818	88.255	63.768	1.00	39.55
ATOM	723	CD	ARG	316	15.004	89.756	63.448	1.00	48.73
ATOM	724	NE	ARG	316	16.369	90.243	63.586	1.00	52.32
ATOM	725	CZ	ARG	316	16.998	90.978	62.676	1.00	54.42
ATOM	726	NH1	ARG	316	16.394	91.330	61.541	1.00	50.05
ATOM	727	NH2	ARG	316	18.259	91.322	62.894	1.00	58.94
ATOM	742	N	ALA	319	14.883	93.183	67.782	1.00	38.65
ATOM	743	CA	ALA	319	14.456	94.164	66.784	1.00	37.22
ATOM	744	C	ALA	319	13.032	94.659	67.106	1.00	39.05
ATOM	745	O	ALA	319	12.794	95.870	67.190	1.00	39.00
ATOM	746	CB	ALA	319	14.501	93.511	65.386	1.00	32.02
ATOM	747	N	VAL	320	12.136	93.697	67.349	1.00	38.72
ATOM	748	CA	VAL	320	10.729	93.930	67.668	1.00	36.93
ATOM	749	C	VAL	320	10.454	94.147	69.180	1.00	35.57
ATOM	750	O	VAL	320	11.296	93.850	70.048	1.00	34.97
ATOM	751	CB	VAL	320	9.889	92.710	67.153	1.00	36.85

ATOM	752	CG1	VAL	320	8.391	92.969	67.218	1.00	36.58
ATOM	753	CG2	VAL	320	10.290	92.405	65.769	1.00	30.70
ATOM	804	N	THR	328	10.898	82.215	58.897	1.00	32.35
ATOM	805	CA	THR	328	9.845	82.464	57.948	1.00	31.40
ATOM	806	C	THR	328	9.676	84.002	57.703	1.00	33.59
ATOM	807	O	THR	328	9.033	84.413	56.733	1.00	35.22
ATOM	808	CB	THR	328	8.589	81.753	58.558	1.00	32.98
ATOM	809	OG1	THR	328	8.351	80.528	57.867	1.00	36.33
ATOM	810	CG2	THR	328	7.338	82.602	58.627	1.00	25.48
ATOM	1105	N	LEU	367	26.072	85.794	70.190	1.00	29.24
ATOM	1106	CA	LEU	367	24.948	84.884	69.994	1.00	25.60
ATOM	1107	C	LEU	367	25.327	83.579	69.317	1.00	25.61
ATOM	1108	O	LEU	367	24.886	82.513	69.740	1.00	28.03
ATOM	1109	CB	LEU	367	23.859	85.522	69.186	1.00	20.56
ATOM	1110	CG	LEU	367	22.788	84.450	69.066	1.00	23.00
ATOM	1111	CD1	LEU	367	21.733	84.549	70.133	1.00	15.44
ATOM	1112	CD2	LEU	367	22.171	84.596	67.721	1.00	30.25
ATOM	1113	N	GLY	368	26.089	83.666	68.236	1.00	22.75
ATOM	1114	CA	GLY	368	26.500	82.469	67.527	1.00	22.27
ATOM	1115	C	GLY	368	27.456	81.654	68.379	1.00	25.34
ATOM	1116	O	GLY	368	27.631	80.443	68.181	1.00	24.00
ATOM	1131	N	ARG	371	25.241	79.722	71.035	1.00	29.43
ATOM	1132	CA	ARG	371	24.712	78.642	70.217	1.00	26.92
ATOM	1133	C	ARG	371	25.781	77.585	69.780	1.00	26.81
ATOM	1134	O	ARG	371	25.428	76.471	69.408	1.00	30.58
ATOM	1135	CB	ARG	371	24.030	79.225	68.995	1.00	26.56
ATOM	1136	CG	ARG	371	22.802	80.020	69.279	1.00	22.05
ATOM	1137	CD	ARG	371	22.202	80.545	67.941	1.00	26.82
ATOM	1138	NE	ARG	371	21.109	79.777	67.318	1.00	24.69
ATOM	1139	CZ	ARG	371	21.216	79.073	66.183	1.00	26.53
ATOM	1140	NH1	ARG	371	22.380	78.996	65.522	1.00	18.75
ATOM	1141	NH2	ARG	371	20.123	78.507	65.645	1.00	23.91

TRbeta Site II Residues (ref. 1BSX.pdb)

ATOM	120	N	THR	A 226	30.851	22.267	38.045	1.00	49.68
ATOM	121	CA	THR	A 226	30.531	21.932	36.661	1.00	49.68
ATOM	122	C	THR	A 226	29.159	21.297	36.533	1.00	49.68
ATOM	123	O	THR	A 226	28.301	21.819	35.826	1.00	49.68

ATOM	124	CB	THR	A	226	31.553	20.961	36.055	1.00 41.41
ATOM	125	OG1	THR	A	226	32.808	21.630	35.883	1.00 41.41
ATOM	126	CG2	THR	A	226	31.059	20.454	34.711	1.00 41.41
ATOM	127	N	GLU	A	227	28.955	20.163	37.198	1.00 52.18
ATOM	128	CA	GLU	A	227	27.657	19.492	37.138	1.00 52.18
ATOM	129	C	GLU	A	227	26.572	20.555	37.274	1.00 52.18
ATOM	130	O	GLU	A	227	25.504	20.453	36.666	1.00 52.18
ATOM	131	CB	GLU	A	227	27.531	18.460	38.266	1.00 51.55
ATOM	132	N	ALA	A	228	26.867	21.584	38.065	1.00 48.32
ATOM	133	CA	ALA	A	228	25.931	22.674	38.278	1.00 48.32
ATOM	134	C	ALA	A	228	25.789	23.508	37.019	1.00 48.32
ATOM	135	O	ALA	A	228	24.795	23.399	36.306	1.00 48.32
ATOM	136	CB	ALA	A	228	26.399	23.543	39.421	1.00 41.74
ATOM	137	N	HIS	A	229	26.788	24.332	36.732	1.00 50.10
ATOM	138	CA	HIS	A	229	26.723	25.177	35.548	1.00 50.10
ATOM	139	C	HIS	A	229	26.203	24.491	34.305	1.00 50.10
ATOM	140	O	HIS	A	229	25.567	25.131	33.479	1.00 50.10
ATOM	141	CB	HIS	A	229	28.087	25.785	35.210	1.00 43.42
ATOM	142	CG	HIS	A	229	28.138	26.393	33.838	1.00 43.42
ATOM	143	ND1	HIS	A	229	27.215	27.315	33.403	1.00 43.42
ATOM	144	CD2	HIS	A	229	28.981	26.180	32.800	1.00 43.42
ATOM	145	CE1	HIS	A	229	27.485	27.645	32.150	1.00 43.42
ATOM	146	NE2	HIS	A	229	28.551	26.971	31.762	1.00 43.42
ATOM	147	N	VAL	A	230	26.475	23.201	34.162	1.00 55.78
ATOM	148	CA	VAL	A	230	26.036	22.498	32.969	1.00 55.78
ATOM	149	C	VAL	A	230	24.555	22.163	32.958	1.00 55.78
ATOM	150	O	VAL	A	230	23.905	22.238	31.914	1.00 55.78
ATOM	151	CB	VAL	A	230	26.812	21.196	32.761	1.00 55.57
ATOM	152	CG1	VAL	A	230	26.472	20.625	31.395	1.00 55.57
ATOM	153	CG2	VAL	A	230	28.295	21.453	32.874	1.00 55.57
ATOM	154	N	ALA	A	231	24.023	21.785	34.112	1.00 61.34
ATOM	155	CA	ALA	A	231	22.614	21.450	34.198	1.00 61.34
ATOM	156	C	ALA	A	231	21.787	22.725	34.312	1.00 61.34
ATOM	157	O	ALA	A	231	20.560	22.675	34.303	1.00 61.34
ATOM	158	CB	ALA	A	231	22.368	20.557	35.394	1.00 58.57
ATOM	159	N	THR	A	232	22.463	23.866	34.408	1.00 57.34
ATOM	160	CA	THR	A	232	21.773	25.145	34.532	1.00 57.34
ATOM	161	C	THR	A	232	22.150	26.114	33.426	1.00 57.34
ATOM	162	O	THR	A	232	21.941	27.315	33.561	1.00 57.34
ATOM	163	CB	THR	A	232	22.099	25.859	35.854	1.00 50.43

ATOM	164	OG1	THR	A	232	23.454	26.318	35.822	1.00	50.43
ATOM	165	CG2	THR	A	232	21.927	24.918	37.026	1.00	50.43
ATOM	166	N	ASN	A	233	22.727	25.604	32.347	1.00	73.93
ATOM	167	CA	ASN	A	233	23.115	26.458	31.234	1.00	73.93
ATOM	168	C	ASN	A	233	22.217	26.033	30.085	1.00	73.93
ATOM	169	O	ASN	A	233	22.240	24.876	29.673	1.00	73.93
ATOM	170	CB	ASN	A	233	24.593	26.254	30.897	1.00	81.13
ATOM	171	CG	ASN	A	233	25.110	27.263	29.895	1.00	81.13
ATOM	172	OD1	ASN	A	233	24.893	28.463	30.034	1.00	81.13
ATOM	173	ND2	ASN	A	233	25.822	26.779	28.888	1.00	81.13
ATOM	174	N	ALA	A	234	21.423	26.971	29.584	1.00	85.48
ATOM	175	CA	ALA	A	234	20.464	26.693	28.526	1.00	85.48
ATOM	176	C	ALA	A	234	20.981	26.046	27.264	1.00	85.48
ATOM	177	O	ALA	A	234	21.988	26.456	26.703	1.00	85.48
ATOM	178	CB	ALA	A	234	19.718	27.958	28.161	1.00	84.92
ATOM	179	N	GLN	A	235	20.249	25.029	26.827	1.00	89.64
ATOM	180	CA	GLN	A	235	20.566	24.303	25.612	1.00	89.64
ATOM	181	C	GLN	A	235	21.961	23.679	25.535	1.00	89.64
ATOM	182	O	GLN	A	235	22.338	23.154	24.489	1.00	89.64
ATOM	183	CB	GLN	A	235	20.336	25.224	24.399	1.00	92.63
ATOM	184	CG	GLN	A	235	18.884	25.361	23.918	1.00	92.63
ATOM	185	CD	GLN	A	235	17.879	25.531	25.043	1.00	92.63
ATOM	186	OE1	GLN	A	235	17.649	24.611	25.825	1.00	92.63
ATOM	187	NE2	GLN	A	235	17.274	26.712	25.128	1.00	92.63
ATOM	429	N	ILE	A	275	11.867	37.044	28.524	1.00	66.16
ATOM	430	CA	ILE	A	275	12.617	35.819	28.794	1.00	66.16
ATOM	431	C	ILE	A	275	13.556	35.932	29.996	1.00	66.16
ATOM	432	O	ILE	A	275	14.025	34.929	30.527	1.00	66.16
ATOM	433	CB	ILE	A	275	13.441	35.398	27.562	1.00	58.27
ATOM	434	CG1	ILE	A	275	14.324	36.551	27.107	1.00	58.27
ATOM	435	CG2	ILE	A	275	12.519	34.972	26.444	1.00	58.27
ATOM	436	CD1	ILE	A	275	15.091	36.244	25.857	1.00	58.27
ATOM	437	N	ILE	A	276	13.815	37.158	30.429	1.00	66.14
ATOM	438	CA	ILE	A	276	14.706	37.417	31.553	1.00	66.14
ATOM	439	C	ILE	A	276	14.296	36.685	32.827	1.00	66.14
ATOM	440	O	ILE	A	276	15.089	36.539	33.750	1.00	66.14
ATOM	441	CB	ILE	A	276	14.737	38.915	31.859	1.00	69.98
ATOM	442	CG1	ILE	A	276	15.765	39.220	32.948	1.00	69.98
ATOM	443	CG2	ILE	A	276	13.369	39.364	32.318	1.00	69.98
ATOM	444	CD1	ILE	A	276	17.177	38.987	32.517	1.00	69.98

ATOM	459	N	ALA	A	279	15.631	33.064	33.124	1.00 47.85
ATOM	460	CA	ALA	A	279	17.065	33.172	33.057	1.00 47.85
ATOM	461	C	ALA	A	279	17.588	33.271	34.468	1.00 47.85
ATOM	462	O	ALA	A	279	18.519	32.561	34.851	1.00 47.85
ATOM	463	CB	ALA	A	279	17.440	34.378	32.279	1.00 44.05
ATOM	464	N	ILE	A	280	16.968	34.144	35.251	1.00 44.23
ATOM	465	CA	ILE	A	280	17.392	34.322	36.623	1.00 44.23
ATOM	466	C	ILE	A	280	17.201	33.025	37.392	1.00 44.23
ATOM	467	O	ILE	A	280	18.088	32.606	38.133	1.00 44.23
ATOM	468	CB	ILE	A	280	16.616	35.455	37.297	1.00 39.34
ATOM	469	CG1	ILE	A	280	16.852	36.757	36.541	1.00 39.34
ATOM	470	CG2	ILE	A	280	17.062	35.605	38.721	1.00 39.34
ATOM	471	CD1	ILE	A	280	16.284	37.966	37.238	1.00 39.34
ATOM	472	N	THR	A	281	16.059	32.375	37.189	1.00 43.46
ATOM	473	CA	THR	A	281	15.792	31.119	37.879	1.00 43.46
ATOM	474	C	THR	A	281	16.976	30.173	37.710	1.00 43.46
ATOM	475	O	THR	A	281	17.415	29.548	38.680	1.00 43.46
ATOM	476	CB	THR	A	281	14.519	30.404	37.347	1.00 52.33
ATOM	477	OG1	THR	A	281	14.671	30.149	35.948	1.00 52.33
ATOM	478	CG2	THR	A	281	13.280	31.252	37.562	1.00 52.33
ATOM	479	N	ARG	A	282	17.495	30.071	36.486	1.00 47.94
ATOM	480	CA	ARG	A	282	18.634	29.199	36.202	1.00 47.94
ATOM	481	C	ARG	A	282	19.775	29.579	37.128	1.00 47.94
ATOM	482	O	ARG	A	282	20.358	28.732	37.806	1.00 47.94
ATOM	483	CB	ARG	A	282	19.099	29.381	34.765	1.00 74.21
ATOM	484	CG	ARG	A	282	19.187	28.100	33.973	1.00 74.21
ATOM	485	CD	ARG	A	282	18.007	27.962	33.025	1.00 74.21
ATOM	486	NE	ARG	A	282	17.893	29.117	32.136	1.00 74.21
ATOM	487	CZ	ARG	A	282	18.885	29.602	31.390	1.00 74.21
ATOM	488	NH1	ARG	A	282	20.093	29.045	31.411	1.00 74.21
ATOM	489	NH2	ARG	A	282	18.675	30.670	30.633	1.00 74.21
ATOM	490	N	VAL	A	283	20.092	30.868	37.138	1.00 45.45
ATOM	491	CA	VAL	A	283	21.142	31.375	37.990	1.00 45.45
ATOM	492	C	VAL	A	283	20.852	30.908	39.405	1.00 45.45
ATOM	493	O	VAL	A	283	21.743	30.458	40.112	1.00 45.45
ATOM	494	CB	VAL	A	283	21.170	32.895	37.957	1.00 42.13
ATOM	495	CG1	VAL	A	283	22.286	33.411	38.849	1.00 42.13
ATOM	496	CG2	VAL	A	283	21.361	33.358	36.533	1.00 42.13
ATOM	497	N	VAL	A	284	19.597	31.008	39.822	1.00 42.56
ATOM	498	CA	VAL	A	284	19.247	30.549	41.157	1.00 42.56

ATOM	499	C	VAL	A	284	19.516	29.042	41.234	1.00 42.56
ATOM	500	O	VAL	A	284	20.202	28.575	42.140	1.00 42.56
ATOM	501	CB	VAL	A	284	17.762	30.790	41.492	1.00 42.15
ATOM	502	CG1	VAL	A	284	17.499	30.381	42.909	1.00 42.15
ATOM	503	CG2	VAL	A	284	17.416	32.242	41.313	1.00 42.15
ATOM	504	N	ASP	A	285	18.987	28.283	40.277	1.00 48.17
ATOM	505	CA	ASP	A	285	19.197	26.843	40.267	1.00 48.17
ATOM	506	C	ASP	A	285	20.676	26.473	40.291	1.00 48.17
ATOM	507	O	ASP	A	285	21.044	25.441	40.846	1.00 48.17
ATOM	508	CB	ASP	A	285	18.522	26.204	39.051	1.00 48.63
ATOM	509	CG	ASP	A	285	17.005	26.271	39.122	1.00 48.63
ATOM	510	OD1	ASP	A	285	16.432	25.721	40.086	1.00 48.63
ATOM	511	OD2	ASP	A	285	16.381	26.865	38.212	1.00 48.63
ATOM	512	N	PHE	A	286	21.522	27.308	39.694	1.00 49.87
ATOM	513	CA	PHE	A	286	22.954	27.030	39.687	1.00 49.87
ATOM	514	C	PHE	A	286	23.543	27.124	41.087	1.00 49.87
ATOM	515	O	PHE	A	286	24.226	26.213	41.538	1.00 49.87
ATOM	516	CB	PHE	A	286	23.687	27.997	38.760	1.00 50.22
ATOM	517	CG	PHE	A	286	25.176	28.000	38.940	1.00 50.22
ATOM	518	CD1	PHE	A	286	25.906	26.828	38.855	1.00 50.22
ATOM	519	CD2	PHE	A	286	25.843	29.186	39.197	1.00 50.22
ATOM	520	CE1	PHE	A	286	27.283	26.841	39.025	1.00 50.22
ATOM	521	CE2	PHE	A	286	27.214	29.210	39.367	1.00 50.22
ATOM	522	CZ	PHE	A	286	27.937	28.038	39.284	1.00 50.22
ATOM	687	N	CYS	A	308	25.191	39.069	42.212	1.00 44.63
ATOM	688	CA	CYS	A	308	25.837	38.359	41.123	1.00 44.63
ATOM	689	C	CYS	A	308	24.900	37.906	40.016	1.00 44.63
ATOM	690	O	CYS	A	308	25.366	37.375	39.015	1.00 44.63
ATOM	691	CB	CYS	A	308	26.554	37.125	41.658	1.00 42.54
ATOM	692	SG	CYS	A	308	25.409	35.829	42.131	1.00 42.54
ATOM	693	N	CYS	A	309	23.595	38.101	40.167	1.00 41.98
ATOM	694	CA	CYS	A	309	22.708	37.618	39.121	1.00 41.98
ATOM	695	C	CYS	A	309	23.019	38.142	37.746	1.00 41.98
ATOM	696	O	CYS	A	309	23.149	37.369	36.805	1.00 41.98
ATOM	697	CB	CYS	A	309	21.257	37.924	39.404	1.00 47.81
ATOM	698	SG	CYS	A	309	20.268	37.272	38.051	1.00 47.81
ATOM	699	N	MET	A	310	23.111	39.456	37.611	1.00 40.05
ATOM	700	CA	MET	A	310	23.419	40.020	36.308	1.00 40.05
ATOM	701	C	MET	A	310	24.800	39.539	35.896	1.00 40.05
ATOM	702	O	MET	A	310	24.988	39.040	34.788	1.00 40.05

ATOM	703	CB	MET	A	310	23.387	41.553	36.357	1.00 39.89
ATOM	704	CG	MET	A	310	23.777	42.209	35.045	1.00 39.89
ATOM	705	SD	MET	A	310	22.737	41.646	33.699	1.00 39.89
ATOM	706	CE	MET	A	310	23.594	42.336	32.298	1.00 39.89
ATOM	707	N	GLU	A	311	25.756	39.668	36.814	1.00 40.89
ATOM	708	CA	GLU	A	311	27.134	39.274	36.565	1.00 40.89
ATOM	709	C	GLU	A	311	27.213	37.868	35.958	1.00 40.89
ATOM	710	O	GLU	A	311	27.864	37.673	34.929	1.00 40.89
ATOM	711	CB	GLU	A	311	27.940	39.357	37.866	1.00 37.60
ATOM	712	CG	GLU	A	311	27.708	40.646	38.645	1.00 37.60
ATOM	713	CD	GLU	A	311	28.590	40.779	39.885	1.00 37.60
ATOM	714	OE1	GLU	A	311	28.752	39.789	40.629	1.00 37.60
ATOM	715	OE2	GLU	A	311	29.112	41.888	40.139	1.00 37.60
ATOM	716	N	ILE	A	312	26.536	36.896	36.566	1.00 40.84
ATOM	717	CA	ILE	A	312	26.569	35.533	36.035	1.00 40.84
ATOM	718	C	ILE	A	312	25.827	35.408	34.707	1.00 40.84
ATOM	719	O	ILE	A	312	26.255	34.664	33.825	1.00 40.84
ATOM	720	CB	ILE	A	312	25.983	34.485	37.033	1.00 34.15
ATOM	721	CG1	ILE	A	312	26.836	34.423	38.306	1.00 34.15
ATOM	722	CG2	ILE	A	312	25.970	33.106	36.388	1.00 34.15
ATOM	723	CD1	ILE	A	312	26.350	33.418	39.331	1.00 34.15
ATOM	724	N	MET	A	313	24.718	36.131	34.558	1.00 41.96
ATOM	725	CA	MET	A	313	23.961	36.071	33.312	1.00 41.96
ATOM	726	C	MET	A	313	24.773	36.591	32.138	1.00 41.96
ATOM	727	O	MET	A	313	25.071	35.834	31.216	1.00 41.96
ATOM	728	CB	MET	A	313	22.635	36.843	33.423	1.00 52.96
ATOM	729	CG	MET	A	313	21.562	36.115	34.245	1.00 52.96
ATOM	730	SD	MET	A	313	19.862	36.769	34.098	1.00 52.96
ATOM	731	CE	MET	A	313	20.065	38.413	34.741	1.00 52.96
ATOM	732	N	SER	A	314	25.141	37.872	32.175	1.00 38.33
ATOM	733	CA	SER	A	314	25.928	38.462	31.094	1.00 38.33
ATOM	734	C	SER	A	314	27.198	37.658	30.774	1.00 38.33
ATOM	735	O	SER	A	314	27.604	37.587	29.616	1.00 38.33
ATOM	736	CB	SER	A	314	26.266	39.927	31.408	1.00 50.03
ATOM	737	OG	SER	A	314	26.887	40.065	32.665	1.00 50.03
ATOM	738	N	LEU	A	315	27.832	37.056	31.781	1.00 38.47
ATOM	739	CA	LEU	A	315	29.017	36.237	31.501	1.00 38.47
ATOM	740	C	LEU	A	315	28.558	35.167	30.527	1.00 38.47
ATOM	741	O	LEU	A	315	29.058	35.052	29.406	1.00 38.47
ATOM	742	CB	LEU	A	315	29.557	35.548	32.769	1.00 31.33

ATOM	743	CG	LEU	A	315	30.628	34.464	32.514	1.00 31.33
ATOM	744	CD1	LEU	A	315	31.827	35.048	31.781	1.00 31.33
ATOM	745	CD2	LEU	A	315	31.073	33.845	33.830	1.00 31.33
ATOM	746	N	ARG	A	316	27.572	34.405	30.981	1.00 42.55
ATOM	747	CA	ARG	A	316	26.994	33.320	30.217	1.00 42.55
ATOM	748	C	ARG	A	316	26.637	33.669	28.803	1.00 42.55
ATOM	749	O	ARG	A	316	26.555	32.788	27.963	1.00 42.55
ATOM	750	CB	ARG	A	316	25.752	32.799	30.916	1.00 40.97
ATOM	751	CG	ARG	A	316	26.060	32.162	32.237	1.00 40.97
ATOM	752	CD	ARG	A	316	24.851	31.475	32.762	1.00 40.97
ATOM	753	NE	ARG	A	316	25.222	30.313	33.542	1.00 40.97
ATOM	754	CZ	ARG	A	316	24.347	29.411	33.946	1.00 40.97
ATOM	755	NH1	ARG	A	316	23.068	29.558	33.631	1.00 40.97
ATOM	756	NH2	ARG	A	316	24.750	28.354	34.634	1.00 40.97
ATOM	767	N	VAL	A	319	30.221	34.487	26.650	1.00 50.27
ATOM	768	CA	VAL	A	319	30.869	33.230	26.290	1.00 50.27
ATOM	769	C	VAL	A	319	30.179	32.610	25.100	1.00 50.27
ATOM	770	O	VAL	A	319	30.602	31.575	24.606	1.00 50.27
ATOM	771	CB	VAL	A	319	30.823	32.209	27.430	1.00 43.16
ATOM	772	CG1	VAL	A	319	31.272	32.861	28.722	1.00 43.16
ATOM	773	CG2	VAL	A	319	29.432	31.637	27.550	1.00 43.16
ATOM	774	N	ARG	A	320	29.110	33.252	24.652	1.00 54.91
ATOM	775	CA	ARG	A	320	28.355	32.781	23.510	1.00 54.91
ATOM	776	C	ARG	A	320	28.265	33.790	22.377	1.00 54.91
ATOM	777	O	ARG	A	320	27.257	33.876	21.680	1.00 54.91
ATOM	778	CB	ARG	A	320	26.968	32.356	23.958	1.00 63.84
ATOM	779	CG	ARG	A	320	26.891	30.895	24.301	1.00 63.84
ATOM	780	CD	ARG	A	320	25.569	30.557	24.916	1.00 63.84
ATOM	781	NE	ARG	A	320	25.330	29.123	24.908	1.00 63.84
ATOM	782	CZ	ARG	A	320	24.358	28.541	25.594	1.00 63.84
ATOM	783	NH1	ARG	A	320	23.552	29.283	26.341	1.00 63.84
ATOM	784	NH2	ARG	A	320	24.177	27.230	25.517	1.00 63.84
ATOM	797	N	ASP	A	322	29.281	34.908	18.810	1.00 58.89
ATOM	798	CA	ASP	A	322	29.780	34.397	17.537	1.00 58.89
ATOM	799	C	ASP	A	322	30.428	35.585	16.827	1.00 58.89
ATOM	800	O	ASP	A	322	29.729	36.503	16.396	1.00 58.89
ATOM	801	CB	ASP	A	322	28.614	33.892	16.678	1.00 55.15
ATOM	802	CG	ASP	A	322	29.068	33.304	15.347	1.00 55.15
ATOM	803	OD1	ASP	A	322	30.036	33.842	14.755	1.00 55.15
ATOM	804	OD2	ASP	A	322	28.439	32.323	14.884	1.00 55.15

ATOM	805	N	PRO	A	323	31.770	35.612	16.709	1.00 61.57
ATOM	806	CA	PRO	A	323	32.317	36.775	16.017	1.00 61.57
ATOM	807	C	PRO	A	323	31.913	36.892	14.533	1.00 61.57
ATOM	808	O	PRO	A	323	31.828	38.003	14.009	1.00 61.57
ATOM	809	CB	PRO	A	323	33.815	36.566	16.199	1.00 58.50
ATOM	810	CG	PRO	A	323	33.915	35.076	16.059	1.00 58.50
ATOM	811	CD	PRO	A	323	32.892	34.762	17.138	1.00 58.50
ATOM	812	N	GLU	A	324	31.698	35.772	13.842	1.00 69.24
ATOM	813	CA	GLU	A	324	31.296	35.868	12.438	1.00 69.24
ATOM	814	C	GLU	A	324	30.010	36.700	12.397	1.00 69.24
ATOM	815	O	GLU	A	324	30.041	37.868	12.016	1.00 69.24
ATOM	816	CB	GLU	A	324	31.039	34.482	11.809	1.00 56.60
ATOM	817	CG	GLU	A	324	32.215	33.479	11.837	1.00 56.60
ATOM	818	CD	GLU	A	324	33.545	34.037	11.313	1.00 56.60
ATOM	819	OE1	GLU	A	324	33.521	34.931	10.433	1.00 56.60
ATOM	820	OE2	GLU	A	324	34.620	33.556	11.761	1.00 56.60
ATOM	874	N	GLY	A	332	20.090	31.110	25.121	1.00 73.02
ATOM	875	CA	GLY	A	332	20.316	30.023	24.190	1.00 73.02
ATOM	876	C	GLY	A	332	19.274	29.921	23.092	1.00 73.02
ATOM	877	O	GLY	A	332	19.303	28.984	22.297	1.00 73.02
ATOM	1148	N	VAL	A	370	34.003	28.455	32.872	1.00 40.00
ATOM	1149	CA	VAL	A	370	32.879	29.368	32.981	1.00 40.00
ATOM	1150	C	VAL	A	370	32.280	29.144	34.357	1.00 40.00
ATOM	1151	O	VAL	A	370	32.101	30.082	35.129	1.00 40.00
ATOM	1152	CB	VAL	A	370	31.778	29.065	31.943	1.00 37.32
ATOM	1153	CG1	VAL	A	370	30.607	29.997	32.157	1.00 37.32
ATOM	1154	CG2	VAL	A	370	32.327	29.220	30.542	1.00 37.32
ATOM	1155	N	ALA	A	371	31.993	27.882	34.655	1.00 37.67
ATOM	1156	CA	ALA	A	371	31.407	27.503	35.927	1.00 37.67
ATOM	1157	C	ALA	A	371	32.165	28.154	37.072	1.00 37.67
ATOM	1158	O	ALA	A	371	31.621	28.990	37.784	1.00 37.67
ATOM	1159	CB	ALA	A	371	31.418	25.989	36.075	1.00 32.11
ATOM	1176	N	GLN	A	374	31.828	31.691	37.341	1.00 36.73
ATOM	1177	CA	GLN	A	374	30.505	32.029	37.866	1.00 36.73
ATOM	1178	C	GLN	A	374	30.426	31.946	39.387	1.00 36.73
ATOM	1179	O	GLN	A	374	29.713	32.733	40.017	1.00 36.73
ATOM	1180	CB	GLN	A	374	29.428	31.110	37.293	1.00 37.11
ATOM	1181	CG	GLN	A	374	29.254	31.181	35.797	1.00 37.11
ATOM	1182	CD	GLN	A	374	28.133	30.278	35.318	1.00 37.11
ATOM	1183	OE1	GLN	A	374	27.860	30.179	34.121	1.00 37.11

ATOM 1184 NE2 GLN A 374 27.476 29.614 36.257 1.00 37.11

VitDR Site II Residues (ref. 1DB1.pdb)

ATOM 134 N LEU A 136 20.223 7.725 47.913 1.00 22.40
ATOM 135 CA LEU A 136 20.991 7.675 46.669 1.00 23.29
ATOM 136 C LEU A 136 20.302 6.721 45.705 1.00 23.50
ATOM 137 O LEU A 136 20.191 6.996 44.512 1.00 23.31
ATOM 138 CB LEU A 136 22.424 7.194 46.920 1.00 24.60
ATOM 139 CG LEU A 136 23.395 8.196 47.549 1.00 25.56
ATOM 140 CD1 LEU A 136 24.740 7.518 47.798 1.00 26.67
ATOM 141 CD2 LEU A 136 23.555 9.398 46.628 1.00 26.04
ATOM 142 N ASP A 137 19.845 5.591 46.232 1.00 23.87
ATOM 143 CA ASP A 137 19.156 4.589 45.427 1.00 23.95
ATOM 144 C ASP A 137 17.844 5.152 44.870 1.00 23.67
ATOM 145 O ASP A 137 17.513 4.943 43.697 1.00 22.79
ATOM 146 CB ASP A 137 18.886 3.348 46.282 1.00 26.93
ATOM 147 CG ASP A 137 18.158 2.266 45.524 1.00 31.10
ATOM 148 OD1 ASP A 137 17.010 1.947 45.900 1.00 34.78
ATOM 149 OD2 ASP A 137 18.730 1.734 44.552 1.00 34.13
ATOM 150 N ALA A 138 17.105 5.867 45.714 1.00 22.31
ATOM 151 CA ALA A 138 15.836 6.472 45.312 1.00 22.31
ATOM 152 C ALA A 138 16.063 7.435 44.157 1.00 21.39
ATOM 153 O ALA A 138 15.310 7.445 43.183 1.00 20.83
ATOM 154 CB ALA A 138 15.213 7.219 46.487 1.00 23.04
ATOM 155 N HIS A 139 17.107 8.249 44.263 1.00 21.06
ATOM 156 CA HIS A 139 17.408 9.202 43.208 1.00 21.28
ATOM 157 C HIS A 139 17.814 8.511 41.905 1.00 21.64
ATOM 158 O HIS A 139 17.385 8.913 40.824 1.00 21.17
ATOM 159 CB HIS A 139 18.528 10.152 43.631 1.00 21.21
ATOM 160 CG HIS A 139 18.730 11.288 42.680 1.00 22.53
ATOM 161 ND1 HIS A 139 19.955 11.593 42.126 1.00 25.49
ATOM 162 CD2 HIS A 139 17.850 12.173 42.157 1.00 19.49
ATOM 163 CE1 HIS A 139 19.820 12.615 41.300 1.00 20.82
ATOM 164 NE2 HIS A 139 18.552 12.986 41.301 1.00 23.99
ATOM 165 N HIS A 140 18.650 7.479 42.005 1.00 21.50
ATOM 166 CA HIS A 140 19.099 6.760 40.819 1.00 22.20
ATOM 167 C HIS A 140 17.947 6.088 40.082 1.00 21.95
ATOM 168 O HIS A 140 17.997 5.911 38.861 1.00 21.87

ATOM	169	CB	HIS	A	140	20.153	5.710	41.193	1.00 23.76
ATOM	170	CG	HIS	A	140	21.398	6.291	41.787	1.00 25.80
ATOM	171	ND1	HIS	A	140	21.803	7.585	41.546	1.00 27.26
ATOM	172	CD2	HIS	A	140	22.341	5.745	42.591	1.00 26.22
ATOM	173	CE1	HIS	A	140	22.942	7.814	42.176	1.00 26.08
ATOM	174	NE2	HIS	A	140	23.291	6.714	42.817	1.00 27.71
ATOM	175	N	LYS	A	141	16.908	5.719	40.821	1.00 20.41
ATOM	176	CA	LYS	A	141	15.745	5.071	40.225	1.00 21.89
ATOM	177	C	LYS	A	141	14.746	6.078	39.665	1.00 21.31
ATOM	178	O	LYS	A	141	13.916	5.730	38.832	1.00 22.47
ATOM	179	CB	LYS	A	141	15.031	4.203	41.265	1.00 23.28
ATOM	180	CG	LYS	A	141	15.804	2.960	41.668	1.00 26.83
ATOM	181	CD	LYS	A	141	15.080	2.209	42.771	1.00 30.63
ATOM	182	CE	LYS	A	141	15.781	0.902	43.093	1.00 33.64
ATOM	183	NZ	LYS	A	141	15.122	0.206	44.231	1.00 36.58
ATOM	184	N	THR	A	142	14.840	7.325	40.107	1.00 20.65
ATOM	185	CA	THR	A	142	13.893	8.348	39.664	1.00 20.68
ATOM	186	C	THR	A	142	14.440	9.502	38.833	1.00 20.45
ATOM	187	O	THR	A	142	13.682	10.375	38.420	1.00 20.32
ATOM	188	CB	THR	A	142	13.142	8.935	40.865	1.00 20.48
ATOM	189	OG1	THR	A	142	14.081	9.474	41.805	1.00 18.91
ATOM	190	CG2	THR	A	142	12.326	7.850	41.546	1.00 19.94
ATOM	191	N	TYR	A	143	15.747	9.520	38.595	1.00 20.03
ATOM	192	CA	TYR	A	143	16.342	10.566	37.768	1.00 20.44
ATOM	193	C	TYR	A	143	17.207	9.895	36.706	1.00 20.75
ATOM	194	O	TYR	A	143	18.248	9.323	37.013	1.00 21.56
ATOM	195	CB	TYR	A	143	17.198	11.529	38.610	1.00 20.88
ATOM	196	CG	TYR	A	143	17.673	12.742	37.835	1.00 20.90
ATOM	197	CD1	TYR	A	143	18.721	12.650	36.915	1.00 21.44
ATOM	198	CD2	TYR	A	143	17.048	13.980	37.994	1.00 21.13
ATOM	199	CE1	TYR	A	143	19.132	13.762	36.170	1.00 21.80
ATOM	200	CE2	TYR	A	143	17.449	15.090	37.253	1.00 20.26
ATOM	201	CZ	TYR	A	143	18.487	14.978	36.347	1.00 22.15
ATOM	202	OH	TYR	A	143	18.868	16.077	35.612	1.00 21.28
ATOM	203	N	ASP	A	144	16.750	9.959	35.461	1.00 20.48
ATOM	204	CA	ASP	A	144	17.449	9.365	34.326	1.00 21.36
ATOM	205	C	ASP	A	144	18.428	10.387	33.751	1.00 22.06
ATOM	206	O	ASP	A	144	18.016	11.348	33.102	1.00 21.75
ATOM	207	CB	ASP	A	144	16.412	8.955	33.274	1.00 21.65
ATOM	208	CG	ASP	A	144	17.032	8.481	31.976	1.00 22.22

ATOM	209	OD1	ASP	A	144	18.261	8.286	31.921	1.00 22.12
ATOM	210	OD2	ASP	A	144	16.266	8.294	31.007	1.00 23.20
ATOM	494	N	LEU	A	233	7.228	18.018	30.549	1.00 21.20
ATOM	495	CA	LEU	A	233	8.483	17.785	31.278	1.00 20.50
ATOM	496	C	LEU	A	233	8.267	17.940	32.785	1.00 20.58
ATOM	497	O	LEU	A	233	8.755	17.139	33.587	1.00 18.39
ATOM	498	CB	LEU	A	233	9.565	18.770	30.811	1.00 20.92
ATOM	499	CG	LEU	A	233	10.826	18.839	31.684	1.00 20.96
ATOM	500	CD1	LEU	A	233	11.554	17.502	31.652	1.00 22.15
ATOM	501	CD2	LEU	A	233	11.737	19.969	31.190	1.00 22.47
ATOM	502	N	VAL	A	234	7.539	18.981	33.172	1.00 20.09
ATOM	503	CA	VAL	A	234	7.263	19.217	34.583	1.00 20.15
ATOM	504	C	VAL	A	234	6.320	18.152	35.146	1.00 19.97
ATOM	505	O	VAL	A	234	6.500	17.691	36.268	1.00 19.99
ATOM	506	CB	VAL	A	234	6.665	20.630	34.796	1.00 21.02
ATOM	507	CG1	VAL	A	234	6.104	20.778	36.209	1.00 23.20
ATOM	508	CG2	VAL	A	234	7.754	21.679	34.566	1.00 21.83
ATOM	527	N	SER	A	237	8.241	15.105	35.711	1.00 17.93
ATOM	528	CA	SER	A	237	9.106	15.312	36.868	1.00 18.19
ATOM	529	C	SER	A	237	8.373	15.218	38.199	1.00 18.73
ATOM	530	O	SER	A	237	8.929	14.737	39.184	1.00 19.34
ATOM	531	CB	SER	A	237	9.830	16.654	36.730	1.00 18.72
ATOM	532	OG	SER	A	237	10.648	16.628	35.573	1.00 19.76
ATOM	533	N	ILE	A	238	7.128	15.680	38.237	1.00 18.89
ATOM	534	CA	ILE	A	238	6.343	15.597	39.460	1.00 20.25
ATOM	535	C	ILE	A	238	6.101	14.119	39.759	1.00 20.17
ATOM	536	O	ILE	A	238	6.129	13.705	40.914	1.00 20.62
ATOM	537	CB	ILE	A	238	4.984	16.337	39.317	1.00 21.21
ATOM	538	CG1	ILE	A	238	5.226	17.847	39.236	1.00 23.61
ATOM	539	CG2	ILE	A	238	4.068	16.001	40.502	1.00 23.76
ATOM	540	CD1	ILE	A	238	3.972	18.668	38.937	1.00 24.70
ATOM	541	N	GLN	A	239	5.868	13.315	38.719	1.00 20.04
ATOM	542	CA	GLN	A	239	5.657	11.890	38.936	1.00 19.72
ATOM	543	C	GLN	A	239	6.911	11.261	39.531	1.00 20.24
ATOM	544	O	GLN	A	239	6.823	10.433	40.437	1.00 19.92
ATOM	545	CB	GLN	A	239	5.288	11.178	37.628	1.00 21.35
ATOM	546	CG	GLN	A	239	3.920	11.576	37.086	1.00 21.87
ATOM	547	CD	GLN	A	239	3.487	10.707	35.922	1.00 23.58
ATOM	548	OE1	GLN	A	239	3.092	9.556	36.105	1.00 26.39
ATOM	549	NE2	GLN	A	239	3.568	11.249	34.720	1.00 22.31

ATOM	550	N	LYS	A	240	8.080	11.661	39.037	1.00 19.37
ATOM	551	CA	LYS	A	240	9.336	11.116	39.557	1.00 19.49
ATOM	552	C	LYS	A	240	9.575	11.583	40.994	1.00 20.03
ATOM	553	O	LYS	A	240	10.086	10.826	41.826	1.00 20.81
ATOM	554	CB	LYS	A	240	10.509	11.525	38.658	1.00 19.27
ATOM	555	CG	LYS	A	240	10.385	11.015	37.216	1.00 19.70
ATOM	556	CD	LYS	A	240	10.174	9.491	37.165	1.00 20.85
ATOM	557	CE	LYS	A	240	10.201	8.986	35.734	1.00 20.78
ATOM	558	NZ	LYS	A	240	9.919	7.527	35.631	1.00 21.79
ATOM	559	N	VAL	A	241	9.203	12.827	41.284	1.00 19.95
ATOM	560	CA	VAL	A	241	9.355	13.380	42.630	1.00 21.18
ATOM	561	C	VAL	A	241	8.466	12.633	43.621	1.00 22.58
ATOM	562	O	VAL	A	241	8.845	12.418	44.769	1.00 22.01
ATOM	563	CB	VAL	A	241	9.006	14.890	42.658	1.00 22.53
ATOM	564	CG1	VAL	A	241	8.893	15.392	44.104	1.00 23.49
ATOM	565	CG2	VAL	A	241	10.092	15.671	41.929	1.00 22.43
ATOM	566	N	ILE	A	242	7.277	12.237	43.178	1.00 22.44
ATOM	567	CA	ILE	A	242	6.375	11.492	44.052	1.00 23.64
ATOM	568	C	ILE	A	242	7.027	10.157	44.416	1.00 23.45
ATOM	569	O	ILE	A	242	6.987	9.726	45.573	1.00 25.50
ATOM	570	CB	ILE	A	242	5.012	11.255	43.360	1.00 24.32
ATOM	571	CG1	ILE	A	242	4.235	12.575	43.303	1.00 25.64
ATOM	572	CG2	ILE	A	242	4.214	10.186	44.104	1.00 24.95
ATOM	573	CD1	ILE	A	242	3.012	12.540	42.401	1.00 25.41
ATOM	574	N	GLY	A	243	7.652	9.521	43.431	1.00 22.76
ATOM	575	CA	GLY	A	243	8.310	8.246	43.665	1.00 23.14
ATOM	576	C	GLY	A	243	9.491	8.385	44.604	1.00 23.29
ATOM	577	O	GLY	A	243	9.719	7.525	45.454	1.00 24.26
ATOM	578	N	PHE	A	244	10.244	9.471	44.443	1.00 22.21
ATOM	579	CA	PHE	A	244	11.406	9.754	45.287	1.00 23.08
ATOM	580	C	PHE	A	244	10.962	9.960	46.734	1.00 23.33
ATOM	581	O	PHE	A	244	11.509	9.359	47.665	1.00 22.96
ATOM	582	CB	PHE	A	244	12.110	11.023	44.799	1.00 21.55
ATOM	583	CG	PHE	A	244	13.264	11.454	45.663	1.00 23.20
ATOM	584	CD1	PHE	A	244	14.474	10.764	45.632	1.00 25.04
ATOM	585	CD2	PHE	A	244	13.140	12.548	46.516	1.00 24.78
ATOM	586	CE1	PHE	A	244	15.542	11.157	46.437	1.00 25.46
ATOM	587	CE2	PHE	A	244	14.205	12.950	47.327	1.00 24.71
ATOM	588	CZ	PHE	A	244	15.407	12.254	47.286	1.00 24.22
ATOM	753	N	SER	A	266	5.847	21.434	47.757	1.00 25.17

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ATOM    754  CA  SER A 266       7.277  21.412  47.449  1.00 23.91
ATOM    755  C   SER A 266       7.609  21.035  46.011  1.00 23.51
ATOM    756  O   SER A 266       8.749  21.206  45.572  1.00 23.30
ATOM    757  CB  SER A 266       8.001  20.445  48.385  1.00 24.45
ATOM    758  OG  SER A 266       7.656  19.101  48.094  1.00 24.60
ATOM    759  N   ALA A 267       6.619  20.519  45.285  1.00 22.67
ATOM    760  CA  ALA A 267       6.801  20.089  43.898  1.00 23.39
ATOM    761  C   ALA A 267       7.698  20.979  43.040  1.00 23.51
ATOM    762  O   ALA A 267       8.716  20.517  42.515  1.00 23.55
ATOM    763  CB  ALA A 267       5.436  19.938  43.217  1.00 24.51
ATOM    764  N   ILE A 268       7.330  22.247  42.883  1.00 22.01
ATOM    765  CA  ILE A 268       8.132  23.135  42.041  1.00 22.23
ATOM    766  C   ILE A 268       9.539  23.374  42.592  1.00 22.05
ATOM    767  O   ILE A 268      10.494  23.558  41.828  1.00 20.90
ATOM    768  CB  ILE A 268       7.426  24.496  41.811  1.00 23.63
ATOM    769  CG1 ILE A 268       8.097  25.232  40.645  1.00 24.85
ATOM    770  CG2 ILE A 268       7.484  25.354  43.068  1.00 25.18
ATOM    771  CD1 ILE A 268       7.933  24.549  39.303  1.00 25.69
ATOM    772  N   GLU A 269       9.674  23.352  43.911  1.00 20.40
ATOM    773  CA  GLU A 269      10.979  23.561  44.529  1.00 20.63
ATOM    774  C   GLU A 269      11.933  22.402  44.268  1.00 21.33
ATOM    775  O   GLU A 269      13.109  22.620  43.976  1.00 20.99
ATOM    776  CB  GLU A 269      10.823  23.770  46.030  1.00 20.38
ATOM    777  CG  GLU A 269      10.206  25.110  46.396  1.00 22.10
ATOM    778  CD  GLU A 269      10.009  25.261  47.892  1.00 23.72
ATOM    779  OE1 GLU A 269      10.803  24.670  48.656  1.00 22.73
ATOM    780  OE2 GLU A 269       9.067  25.974  48.301  1.00 24.58
ATOM    781  N   VAL A 270      11.434  21.172  44.375  1.00 20.39
ATOM    782  CA  VAL A 270      12.279  20.006  44.143  1.00 20.83
ATOM    783  C   VAL A 270      12.644  19.911  42.670  1.00 20.52
ATOM    784  O   VAL A 270      13.734  19.458  42.318  1.00 20.87
ATOM    785  CB  VAL A 270      11.582  18.709  44.597  1.00 21.55
ATOM    786  CG1 VAL A 270      12.481  17.512  44.318  1.00 21.95
ATOM    787  CG2 VAL A 270      11.268  18.790  46.086  1.00 23.25
ATOM    788  N   ILE A 271      11.731  20.337  41.804  1.00 20.29
ATOM    789  CA  ILE A 271      12.010  20.318  40.376  1.00 20.71
ATOM    790  C   ILE A 271      13.145  21.300  40.099  1.00 20.86
ATOM    791  O   ILE A 271      14.083  20.990  39.361  1.00 20.78
ATOM    792  CB  ILE A 271      10.755  20.684  39.563  1.00 21.89
ATOM    793  CG1 ILE A 271       9.842  19.450  39.483  1.00 24.21
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ATOM	794	CG2	ILE	A	271	11.149	21.173	38.170	1.00 23.03
ATOM	795	CD1	ILE	A	271	8.489	19.711	38.852	1.00 27.85
ATOM	796	N	MET	A	272	13.076	22.481	40.701	1.00 21.17
ATOM	797	CA	MET	A	272	14.147	23.446	40.500	1.00 21.57
ATOM	798	C	MET	A	272	15.474	22.888	41.020	1.00 20.82
ATOM	799	O	MET	A	272	16.513	23.064	40.384	1.00 22.20
ATOM	800	CB	MET	A	272	13.800	24.770	41.183	1.00 22.31
ATOM	801	CG	MET	A	272	12.595	25.441	40.549	1.00 24.16
ATOM	802	SD	MET	A	272	12.222	27.036	41.296	1.00 26.22
ATOM	803	CE	MET	A	272	11.003	27.687	40.134	1.00 26.38
ATOM	804	N	LEU	A	273	15.442	22.204	42.163	1.00 21.17
ATOM	805	CA	LEU	A	273	16.661	21.606	42.717	1.00 21.28
ATOM	806	C	LEU	A	273	17.226	20.486	41.842	1.00 20.96
ATOM	807	O	LEU	A	273	18.408	20.494	41.487	1.00 20.75
ATOM	808	CB	LEU	A	273	16.405	21.026	44.116	1.00 22.98
ATOM	809	CG	LEU	A	273	16.367	21.940	45.337	1.00 25.62
ATOM	810	CD1	LEU	A	273	15.959	21.129	46.572	1.00 25.83
ATOM	811	CD2	LEU	A	273	17.736	22.571	45.543	1.00 26.65
ATOM	812	N	ARG	A	274	16.385	19.517	41.494	1.00 19.69
ATOM	813	CA	ARG	A	274	16.852	18.384	40.702	1.00 19.52
ATOM	814	C	ARG	A	274	17.317	18.787	39.309	1.00 19.10
ATOM	815	O	ARG	A	274	18.159	18.117	38.715	1.00 19.83
ATOM	816	CB	ARG	A	274	15.759	17.299	40.610	1.00 19.75
ATOM	817	CG	ARG	A	274	14.652	17.566	39.601	1.00 19.52
ATOM	818	CD	ARG	A	274	13.381	16.792	39.969	1.00 19.72
ATOM	819	NE	ARG	A	274	13.599	15.356	40.153	1.00 18.11
ATOM	820	CZ	ARG	A	274	13.580	14.453	39.175	1.00 19.01
ATOM	821	NH1	ARG	A	274	13.357	14.824	37.919	1.00 18.53
ATOM	822	NH2	ARG	A	274	13.759	13.168	39.458	1.00 19.51
ATOM	837	N	GLU	A	277	21.096	19.280	38.000	1.00 20.52
ATOM	838	CA	GLU	A	277	21.925	18.226	37.425	1.00 21.75
ATOM	839	C	GLU	A	277	22.103	18.370	35.908	1.00 21.79
ATOM	840	O	GLU	A	277	23.105	17.910	35.351	1.00 22.41
ATOM	841	CB	GLU	A	277	21.331	16.852	37.785	1.00 22.91
ATOM	842	CG	GLU	A	277	22.199	15.659	37.413	1.00 26.24
ATOM	843	CD	GLU	A	277	21.904	14.418	38.261	1.00 28.07
ATOM	844	OE1	GLU	A	277	22.359	13.319	37.875	1.00 30.43
ATOM	845	OE2	GLU	A	277	21.233	14.532	39.317	1.00 26.56
ATOM	846	N	SER	A	278	21.152	19.011	35.234	1.00 19.68
ATOM	847	CA	SER	A	278	21.266	19.194	33.789	1.00 20.64

ATOM	848	C	SER	A	278	21.712	20.607	33.448	1.00 21.58
ATOM	849	O	SER	A	278	22.008	20.910	32.292	1.00 22.05
ATOM	850	CB	SER	A	278	19.934	18.910	33.092	1.00 20.93
ATOM	851	OG	SER	A	278	18.941	19.829	33.497	1.00 22.00
ATOM	863	N	THR	A	280	24.077	23.728	33.010	1.00 24.73
ATOM	864	CA	THR	A	280	25.496	23.872	32.728	1.00 26.87
ATOM	865	C	THR	A	280	25.884	25.343	32.672	1.00 27.44
ATOM	866	O	THR	A	280	25.186	26.162	32.070	1.00 26.28
ATOM	867	CB	THR	A	280	25.897	23.198	31.399	1.00 27.76
ATOM	868	OG1	THR	A	280	27.298	23.408	31.173	1.00 31.72
ATOM	869	CG2	THR	A	280	25.107	23.768	30.236	1.00 27.79
ATOM	870	N	MET	A	281	26.991	25.676	33.326	1.00 28.33
ATOM	871	CA	MET	A	281	27.469	27.049	33.340	1.00 31.03
ATOM	872	C	MET	A	281	28.275	27.390	32.095	1.00 31.28
ATOM	873	O	MET	A	281	28.812	28.490	31.980	1.00 30.87
ATOM	874	CB	MET	A	281	28.298	27.306	34.596	1.00 33.43
ATOM	875	CG	MET	A	281	27.448	27.518	35.835	1.00 36.11
ATOM	876	SD	MET	A	281	28.429	27.829	37.295	1.00 39.85
ATOM	877	CE	MET	A	281	28.995	29.495	36.967	1.00 40.40
ATOM	878	N	ASP	A	282	28.364	26.448	31.159	1.00 31.72
ATOM	879	CA	ASP	A	282	29.097	26.709	29.925	1.00 32.91
ATOM	880	C	ASP	A	282	28.366	27.818	29.175	1.00 32.02
ATOM	881	O	ASP	A	282	28.989	28.764	28.683	1.00 31.15
ATOM	882	CB	ASP	A	282	29.172	25.455	29.050	1.00 35.93
ATOM	883	CG	ASP	A	282	29.947	24.328	29.708	1.00 39.91
ATOM	884	OD1	ASP	A	282	30.940	24.619	30.412	1.00 42.35
ATOM	885	OD2	ASP	A	282	29.573	23.150	29.508	1.00 42.45
ATOM	935	N	GLY	A	289	20.675	16.498	26.466	1.00 37.69
ATOM	936	CA	GLY	A	289	20.897	15.682	25.286	1.00 41.85
ATOM	937	C	GLY	A	289	21.072	16.536	24.044	1.00 44.11
ATOM	938	O	GLY	A	289	21.842	17.497	24.051	1.00 45.10
ATOM	1269	N	HIS	A	330	23.291	16.450	47.721	1.00 22.72
ATOM	1270	CA	HIS	A	330	22.225	16.836	46.803	1.00 22.97
ATOM	1271	C	HIS	A	330	20.908	16.139	47.150	1.00 23.43
ATOM	1272	O	HIS	A	330	19.863	16.790	47.257	1.00 22.10
ATOM	1273	CB	HIS	A	330	22.638	16.494	45.364	1.00 24.13
ATOM	1274	CG	HIS	A	330	21.648	16.916	44.321	1.00 25.22
ATOM	1275	ND1	HIS	A	330	21.357	18.237	44.060	1.00 25.99
ATOM	1276	CD2	HIS	A	330	20.913	16.190	43.444	1.00 25.76
ATOM	1277	CE1	HIS	A	330	20.489	18.307	43.065	1.00 26.73

ATOM	1278	NE2	HIS	A	330	20.203	17.078	42.674	1.00 25.08
ATOM	1279	N	VAL	A	331	20.955	14.823	47.334	1.00 22.22
ATOM	1280	CA	VAL	A	331	19.739	14.072	47.642	1.00 23.00
ATOM	1281	C	VAL	A	331	19.185	14.382	49.024	1.00 22.12
ATOM	1282	O	VAL	A	331	17.968	14.393	49.218	1.00 21.17
ATOM	1283	CB	VAL	A	331	19.952	12.544	47.490	1.00 22.74
ATOM	1284	CG1	VAL	A	331	20.363	12.233	46.053	1.00 25.60
ATOM	1285	CG2	VAL	A	331	21.008	12.045	48.466	1.00 25.97
ATOM	1302	N	MET	A	334	17.198	17.654	48.776	1.00 21.27
ATOM	1303	CA	MET	A	334	15.878	17.513	48.163	1.00 20.93
ATOM	1304	C	MET	A	334	14.928	16.881	49.171	1.00 21.48
ATOM	1305	O	MET	A	334	13.769	17.263	49.256	1.00 21.52
ATOM	1306	CB	MET	A	334	15.939	16.648	46.896	1.00 21.53
ATOM	1307	CG	MET	A	334	16.631	17.318	45.719	1.00 22.31
ATOM	1308	SD	MET	A	334	16.442	16.343	44.219	1.00 24.84
ATOM	1309	CE	MET	A	334	17.484	14.909	44.612	1.00 24.19

Example 23

X-ray Structure Coordinates of GR Site II, Table IV

Below is Table IV, which gives the x-ray structure coordinates for GR Site II discerned from the disclosure in WO 03/015692 A2, February 27, 2003, Apolito, et. al,. The format used is based on that commonly used in the RCSB (Research Collaboratory for Structural Bioinformatics, pdb file format), and the fields listed from left to right are defined as follows: record name, atom serial number, atom name, residue name, chain identifier, residue sequence number, orthogonal coordinate for x in Ångstroms, orthogonal cordinate for y in Ångstroms, orthogonal coordinate for z in Ångstroms, occupancy, and temperature factor.

Table IV

ATOM	1	N	GLU	537	49.171	2.415	43.840	1.00 59.21
ATOM	2	CA	GLU	537	48.231	3.343	43.210	1.00 59.76
ATOM	3	C	GLU	537	47.139	2.698	42.370	1.00 61.66
ATOM	4	O	GLU	537	45.973	3.101	42.430	1.00 60.28
ATOM	5	CB	GLU	537	48.984	4.292	42.300	1.00 59.81
ATOM	6	CG	GLU	537	48.816	5.744	42.620	1.00 60.10
ATOM	7	CD	GLU	537	48.907	6.616	41.380	1.00 64.34

ATOM	8	OE1	GLU	537	47.868	6.813	40.700	1.00	57.41
ATOM	9	OE2	GLU	537	50.024	7.091	41.080	1.00	62.84
ATOM	10	N	VAL	538	47.536	1.717	41.560	1.00	60.48
ATOM	11	CA	VAL	538	46.606	1.045	40.670	1.00	63.41
ATOM	12	C	VAL	538	45.768	-0.046	41.310	1.00	57.99
ATOM	13	O	VAL	538	44.828	-0.530	40.680	1.00	58.71
ATOM	14	CB	VAL	538	47.325	0.448	39.440	1.00	64.15
ATOM	15	CG2	VAL	538	47.973	-0.883	39.790	1.00	63.88
ATOM	16	CG	VAL	538	48.334	1.444	38.900	1.00	60.29
ATOM	17	N	ILK	539	46.094	-0.454	42.530	1.00	61.14
ATOM	18	CA	ILK	539	45.282	-1.484	43.180	1.00	60.23
ATOM	19	C	ILK	539	44.259	-0.811	44.090	1.00	61.40
ATOM	20	O	ILK	539	43.321	-1.447	44.570	1.00	63.49
ATOM	21	CB	ILK	539	46.141	-2.499	44.010	1.00	65.32
ATOM	22	CG2	ILK	539	47.243	-3.066	43.140	1.00	61.32
ATOM	23	CG	ILK	539	46.775	-1.833	45.220	1.00	63.80
ATOM	24	CD1	ILK	539	47.356	-2.833	46.200	1.00	60.85
ATOM	25	N	GLU	540	44.451	0.489	44.310	1.00	61.12
ATOM	26	CA	GLU	540	43.584	1.307	45.153	1.00	60.76
ATOM	27	C	GLU	540	42.169	1.264	44.585	1.00	61.78
ATOM	28	O	GLU	540	41.928	1.709	43.459	1.00	61.36
ATOM	29	CB	GLU	540	44.109	2.753	45.173	1.00	58.26
ATOM	30	CG	GLU	540	43.466	3.684	46.191	1.00	61.15
ATOM	31	CD	GLU	540	43.598	3.183	47.619	1.00	61.95
ATOM	32	OE1	GLU	540	44.656	2.591	47.950	1.00	59.71
ATOM	33	OE2	GLU	540	42.649	3.397	48.410	1.00	62.96
ATOM	34	N	PRO	541	41.214	0.713	45.352	1.00	63.77
ATOM	35	CA	PRO	541	39.830	0.632	44.876	1.00	60.14
ATOM	36	C	PRO	541	39.180	1.991	44.592	1.00	62.36
ATOM	37	O	PRO	541	39.455	2.982	45.283	1.00	59.45
ATOM	38	CB	PRO	541	39.131	-0.149	45.988	1.00	59.62
ATOM	39	CG	PRO	541	39.978	0.122	47.195	1.00	60.56
ATOM	40	CD	PRO	541	41.365	0.053	46.659	1.00	58.98
ATOM	41	N	GLU	542	38.332	2.039	43.563	1.00	60.43
ATOM	42	CA	GLU	542	37.653	3.279	43.198	1.00	62.04
ATOM	43	C	GLU	542	36.548	3.515	44.208	1.00	63.11
ATOM	44	O	GLU	542	35.941	2.564	44.697	1.00	59.70
ATOM	45	CB	GLU	542	37.091	3.201	41.770	1.00	62.84
ATOM	46	CG	GLU	542	36.130	2.050	41.511	1.00	63.24
ATOM	47	CD	GLU	542	35.745	1.911	40.031	1.00	63.39

ATOM	48	OE2	GLU	542	34.568	1.599	39.743	1.00	59.31
ATOM	49	OE	GLU	542	36.622	2.095	39.153	1.00	60.50
ATOM	50	N	VAL	543	36.304	4.783	44.528	1.00	61.53
ATOM	51	CA	VAL	543	35.299	5.148	45.518	1.00	63.47
ATOM	52	C	VAL	543	33.886	4.748	45.126	1.00	61.39
ATOM	53	O	VAL	543	33.495	4.877	43.965	1.00	60.79
ATOM	54	CB	VAL	543	35.334	6.661	45.801	1.00	62.60
ATOM	55	CG1	VAL	543	34.467	6.984	46.987	1.00	60.93
ATOM	56	CG2	VAL	543	36.762	7.103	46.064	1.00	59.59
TER	57		VAL	543					
ATOM	58	N	LEU	566	27.382	0.590	53.462	1.00	62.25
ATOM	59	CA	LEU	566	28.495	1.064	52.656	1.00	60.20
ATOM	60	C	LEU	566	29.756	0.424	53.218	1.00	62.85
ATOM	61	O	LEU	566	30.576	-0.116	52.474	1.00	60.20
ATOM	62	CB	LEU	566	28.596	2.594	52.741	1.00	59.50
ATOM	63	CG	LEU	566	29.801	3.267	52.076	1.00	64.18
ATOM	64	CD1	LEU	566	29.685	3.195	50.565	1.00	61.46
ATOM	65	CD2	LEU	566	29.869	4.700	52.516	1.00	62.10
ATOM	66	N	GLY	567	29.886	0.477	54.542	1.00	59.45
ATOM	67	CA	GLY	567	31.040	-0.095	55.207	1.00	59.94
ATOM	68	C	GLY	567	31.316	-1.516	54.768	1.00	60.71
ATOM	69	O	GLY	567	32.461	-1.890	54.520	1.00	59.79
TER	70		GLY	567					
ATOM	71	N	GLN	570	32.788	-1.713	51.295	1.00	60.73
ATOM	72	CA	GLN	570	34.123	-1.132	51.300	1.00	62.31
ATOM	73	C	GLN	570	35.144	-2.093	51.882	1.00	61.15
ATOM	74	O	GLN	570	36.293	-2.134	51.441	1.00	60.50
ATOM	75	CB	GLN	570	34.143	0.150	52.120	1.00	59.04
ATOM	76	CG	GLN	570	33.608	1.361	51.417	1.00	62.03
ATOM	77	CD	GLN	570	33.782	2.606	52.247	1.00	56.35
ATOM	78	OE1	GLN	570	33.460	3.698	51.801	1.00	62.86
ATOM	79	NE2	GLN	570	34.295	2.449	53.467	1.00	63.17
ATOM	80	N	VAL	571	34.732	-2.837	52.903	1.00	60.99
ATOM	81	CA	VAL	571	35.615	-3.792	53.554	1.00	61.91
ATOM	82	C	VAL	571	35.805	-5.007	52.665	1.00	62.66
ATOM	83	O	VAL	571	36.698	-5.820	52.885	1.00	58.99
ATOM	84	CB	VAL	571	35.054	-4.200	54.930	1.00	58.42
ATOM	85	CG1	VAL	571	35.822	-5.393	55.485	1.00	61.27
ATOM	86	CG2	VAL	571	35.160	-3.007	55.891	1.00	60.58
ATOM	87	N	ILK	572	34.958	-5.116	51.652	1.00	63.61

ATOM	88	CA	ILK	572	35.042	-6.206	50.695	1.00	63.76
ATOM	89	C	ILK	572	35.999	-5.772	49.589	1.00	60.35
ATOM	90	O	ILK	572	36.733	-6.587	49.042	1.00	62.13
ATOM	91	CB	ILK	572	33.649	-6.539	50.103	1.00	60.98
ATOM	92	CG2	ILK	572	33.794	-7.443	48.883	1.00	63.63
ATOM	93	CG1	ILK	572	32.782	-7.192	51.183	1.00	61.03
ATOM	94	CD1	ILK	572	31.346	-7.366	50.801	1.00	62.17
ATOM	95	N	ALA	573	35.984	-4.481	49.265	1.00	62.76
ATOM	96	CA	ALA	573	36.879	-3.936	48.251	1.00	58.47
ATOM	97	C	ALA	573	38.271	-3.997	48.872	1.00	61.14
ATOM	98	O	ALA	573	39.294	-4.088	48.180	1.00	60.46
ATOM	99	CB	ALA	573	36.502	-2.496	47.940	1.00	61.48
ATOM	100	N	ALA	574	38.273	-3.964	50.200	1.00	60.84
ATOM	101	CA	ALA	574	39.477	-4.008	51.003	1.00	61.42
ATOM	102	C	ALA	574	40.294	-5.282	50.771	1.00	58.96
ATOM	103	O	ALA	574	41.506	-5.217	50.518	1.00	61.38
ATOM	104	CB	ALA	574	39.098	-3.888	52.465	1.00	60.18
ATOM	105	N	VAL	575	39.631	-6.435	50.861	1.00	59.99
ATOM	106	CA	VAL	575	40.296	-7.720	50.664	1.00	59.60
ATOM	107	C	VAL	575	41.009	-7.779	49.318	1.00	60.96
ATOM	108	O	VAL	575	42.222	-7.981	49.264	1.00	62.47
ATOM	109	CB	VAL	575	39.309	-8.898	50.732	1.00	56.06
ATOM	110	CG2	VAL	575	38.547	-8.880	52.057	1.00	63.34
ATOM	111	CG	VAL	575	40.070	-10.197	50.570	1.00	62.55
ATOM	112	N	LYS	576	40.265	-7.584	48.236	1.00	59.97
ATOM	113	CA	LYS	576	40.851	-7.628	46.901	1.00	62.25
ATOM	114	C	LYS	576	41.957	-6.593	46.742	1.00	63.69
ATOM	115	O	LYS	576	42.673	-6.573	45.742	1.00	59.32
ATOM	116	CB	LYS	576	39.770	-7.391	45.860	1.00	60.99
ATOM	117	CG	LYS	576	40.115	-7.866	44.462	1.00	61.35
ATOM	118	CD	LYS	576	38.905	-7.708	43.568	1.00	63.13
ATOM	119	CE	LYS	576	37.667	-8.234	44.276	1.00	62.07
ATOM	120	NZ	LYS	576	36.420	-7.912	43.531	1.00	59.76
ATOM	121	N	TRP	577	42.074	-5.723	47.734	1.00	62.59
ATOM	122	CA	TRP	577	43.091	-4.694	47.734	1.00	62.15
ATOM	123	C	TRP	577	44.263	-5.272	48.509	1.00	64.09
ATOM	124	O	TRP	577	45.403	-5.238	48.055	1.00	61.89
ATOM	125	CB	TRP	577	42.556	-3.432	48.424	1.00	60.50
ATOM	126	CG	TRP	577	43.620	-2.458	48.780	1.00	63.03
ATOM	127	CD1	TRP	577	44.346	-1.698	47.924	1.00	62.09

ATOM	128	CD2	TRP	577	44.140	-2.200	50.090	1.00	58.79
ATOM	129	NE1	TRP	577	45.293	-0.983	48.611	1.00	61.93
ATOM	130	CE2	TRP	577	45.189	-1.272	49.945	1.00	64.04
ATOM	131	CE3	TRP	577	43.824	-2.668	51.372	1.00	60.56
ATOM	132	CZ2	TRP	577	45.930	-0.798	51.032	1.00	61.40
ATOM	133	CZ3	TRP	577	44.566	-2.197	52.458	1.00	59.59
ATOM	134	CH2	TRP	577	45.607	-1.271	52.277	1.00	61.92
TER	135		TRP	577					
ATOM	136	N	SER	599	42.278	-4.312	61.305	1.00	58.28
ATOM	137	CA	SER	599	42.491	-2.988	60.774	1.00	62.69
ATOM	138	C	SER	599	41.365	-2.525	59.867	1.00	64.40
ATOM	139	O	SER	599	41.398	-1.405	59.367	1.00	62.40
ATOM	140	CB	SER	599	43.837	-2.949	60.046	1.00	62.55
ATOM	141	OG	SER	599	44.008	-4.083	59.216	1.00	62.72
ATOM	142	N	TRP	600	40.358	-3.375	59.677	1.00	59.48
ATOM	143	CA	TRP	600	39.245	-3.026	58.807	1.00	62.88
ATOM	144	C	TRP	600	38.789	-1.630	59.169	1.00	62.61
ATOM	145	O	TRP	600	38.533	-0.805	58.308	1.00	62.45
ATOM	146	CB	TRP	600	38.073	-4.031	58.932	1.00	64.17
ATOM	147	CG	TRP	600	37.282	-3.951	60.198	1.00	62.02
ATOM	148	CD1	TRP	600	37.583	-4.533	61.395	1.00	58.92
ATOM	149	CD2	TRP	600	36.105	-3.166	60.420	1.00	58.67
ATOM	150	NE1	TRP	600	36.672	-4.151	62.355	1.00	64.28
ATOM	151	CE2	TRP	600	35.754	-3.311	61.781	1.00	61.68
ATOM	152	CE3	TRP	600	35.314	-2.350	59.603	1.00	62.68
ATOM	153	CZ2	TRP	600	34.648	-2.666	62.342	1.00	61.17
ATOM	154	CZ3	TRP	600	34.217	-1.711	60.159	1.00	58.94
ATOM	155	CH2	TRP	600	33.894	-1.871	61.516	1.00	61.08
ATOM	156	N	MET	601	38.744	-1.344	60.458	1.00	63.90
ATOM	157	CA	MET	601	38.298	-0.049	60.884	1.00	60.96
ATOM	158	C	MET	601	39.225	1.129	60.577	1.00	61.08
ATOM	159	O	MET	601	38.758	2.167	60.114	1.00	60.27
ATOM	160	CB	MET	601	37.968	-0.064	62.351	1.00	60.46
ATOM	161	CG	MET	601	37.139	1.112	62.702	1.00	61.28
ATOM	162	SD	MET	601	35.774	1.420	61.631	1.00	59.33
ATOM	163	CE	MET	601	34.684	1.638	62.889	1.00	64.63
ATOM	164	N	SER	602	40.521	0.979	60.854	1.00	61.23
ATOM	165	CA	SER	602	41.488	2.035	60.581	1.00	59.98
ATOM	166	C	SER	602	41.536	2.214	59.079	1.00	60.99
ATOM	167	O	SER	602	41.609	3.327	58.581	1.00	64.11

ATOM	168	CB	SER	602	42.872	1.647	61.083	1.00	60.99
ATOM	169	OG	SER	602	42.783	1.022	62.350	1.00	66.17
ATOM	170	N	LEU	603	41.494	1.108	58.351	1.00	59.44
ATOM	171	CA	LEU	603	41.522	1.185	56.901	1.00	61.46
ATOM	172	C	LEU	603	40.386	2.061	56.408	1.00	60.47
ATOM	173	O	LEU	603	40.599	3.062	55.731	1.00	63.39
ATOM	174	CB	LEU	603	41.402	-0.212	56.280	1.00	59.31
ATOM	175	CG	LEU	603	42.646	-1.097	56.346	1.00	61.54
ATOM	176	CD1	LEU	603	42.415	-2.362	55.549	1.00	63.99
ATOM	177	CD2	LEU	603	43.828	-0.346	55.787	1.00	63.36
ATOM	178	N	MET	604	39.173	1.688	56.784	1.00	63.54
ATOM	179	CA	MET	604	38.000	2.417	56.365	1.00	62.81
ATOM	180	C	MET	604	37.898	3.832	56.856	1.00	60.43
ATOM	181	O	MET	604	37.397	4.695	56.132	1.00	62.37
ATOM	182	CB	MET	604	36.770	1.623	56.723	1.00	58.90
ATOM	183	CG	MET	604	36.632	0.429	55.842	1.00	59.86
ATOM	184	SD	MET	604	37.633	0.438	54.374	1.00	62.53
ATOM	185	CE	MET	604	36.663	-0.510	53.559	1.00	60.72
ATOM	186	N	ALA	605	38.375	4.076	58.072	1.00	59.95
ATOM	187	CA	ALA	605	38.357	5.409	58.664	1.00	60.49
ATOM	188	C	ALA	605	39.381	6.309	57.985	1.00	61.50
ATOM	189	O	ALA	605	39.071	7.427	57.583	1.00	59.82
ATOM	190	CB	ALA	605	38.667	5.317	60.132	1.00	59.15
ATOM	191	N	PHE	606	40.608	5.810	57.870	1.00	63.59
ATOM	192	CA	PHE	606	41.700	6.554	57.258	1.00	60.15
ATOM	193	C	PHE	606	41.362	6.933	55.825	1.00	61.96
ATOM	194	O	PHE	606	41.751	7.991	55.356	1.00	60.07
ATOM	195	CB	PHE	606	42.981	5.713	57.285	1.00	63.75
ATOM	196	CG	PHE	606	44.237	6.490	56.999	1.00	64.30
ATOM	197	CD1	PHE	606	44.723	7.424	57.913	1.00	61.77
ATOM	198	CD2	PHE	606	44.957	6.265	55.829	1.00	60.74
ATOM	199	CE1	PHE	606	45.910	8.118	57.665	1.00	64.00
ATOM	200	CE2	PHE	606	46.145	6.955	55.575	1.00	62.47
ATOM	201	CZ	PHE	606	46.620	7.879	56.496	1.00	63.95
ATOM	202	N	ALA	607	40.644	6.063	55.126	1.00	62.00
ATOM	203	CA	ALA	607	40.264	6.338	53.745	1.00	57.50
ATOM	204	C	ALA	607	39.105	7.324	53.684	1.00	64.88
ATOM	205	O	ALA	607	38.931	8.030	52.703	1.00	59.60
ATOM	206	CB	ALA	607	39.888	5.051	53.039	1.00	59.69
TER	207		ALA	607					

ATOM	208	N	TRP	610	40.835	10.650	54.039	1.00	62.47
ATOM	209	CA	TRP	610	41.488	11.102	52.823	1.00	61.40
ATOM	210	C	TRP	610	40.517	11.797	51.874	1.00	60.80
ATOM	211	O	TRP	610	40.797	12.866	51.358	1.00	60.72
ATOM	212	CB	TRP	610	42.141	9.917	52.123	1.00	62.68
ATOM	213	CG	TRP	610	42.744	10.264	50.817	1.00	62.61
ATOM	214	CD1	TRP	610	42.254	9.965	49.582	1.00	58.08
ATOM	215	CD2	TRP	610	43.955	10.991	50.604	1.00	61.10
ATOM	216	NE1	TRP	610	43.086	10.459	48.608	1.00	62.17
ATOM	217	CE2	TRP	610	44.139	11.095	49.209	1.00	62.45
ATOM	218	CE3	TRP	610	44.906	11.565	51.457	1.00	63.78
ATOM	219	CZ2	TRP	610	45.238	11.751	48.646	1.00	60.53
ATOM	220	CZ3	TRP	610	46.001	12.219	50.896	1.00	62.27
ATOM	221	CH2	TRP	610	46.156	12.305	49.505	1.00	60.31
ATOM	222	N	ARG	611	39.368	11.191	51.639	1.00	61.36
ATOM	223	CA	ARG	611	38.412	11.790	50.738	1.00	58.33
ATOM	224	C	ARG	611	37.898	13.128	51.277	1.00	62.93
ATOM	225	O	ARG	611	37.610	14.051	50.502	1.00	61.13
ATOM	226	CB	ARG	611	37.254	10.817	50.486	1.00	62.33
ATOM	227	CG	ARG	611	37.684	9.490	49.873	1.00	60.18
ATOM	228	CD	ARG	611	36.476	8.686	49.426	1.00	59.83
ATOM	229	NE	ARG	611	35.604	8.333	50.544	1.00	61.17
ATOM	230	CZ	ARG	611	35.817	7.308	51.366	1.00	59.54
ATOM	231	NH1	ARG	611	36.875	6.528	51.187	1.00	61.47
ATOM	232	NH2	ARG	611	34.988	7.072	52.376	1.00	62.25
TER	233		ARG	611					
ATOM	234	N	ARG	614	40.511	15.896	50.745	1.00	61.73
ATOM	235	CA	ARG	614	40.623	16.190	49.328	1.00	61.64
ATOM	236	C	ARG	614	39.440	16.960	48.776	1.00	58.09
ATOM	237	O	ARG	614	39.613	17.922	48.041	1.00	63.07
ATOM	238	CB	ARG	614	40.835	14.880	48.545	1.00	62.80
ATOM	239	CG	ARG	614	42.274	14.328	48.621	1.00	58.30
ATOM	240	CD	ARG	614	42.908	14.348	47.242	1.00	60.57
ATOM	241	NE	ARG	614	44.369	14.448	47.262	1.00	61.63
ATOM	242	CZ	ARG	614	45.056	15.421	47.868	1.00	63.66
ATOM	243	NH1	ARG	614	44.414	16.386	48.521	1.00	61.59
ATOM	244	NH2	ARG	614	46.389	15.451	47.797	1.00	64.70
ATOM	245	N	GLN	615	38.239	16.538	49.137	1.00	64.09
ATOM	246	CA	GLN	615	37.033	17.192	48.660	1.00	61.67
ATOM	247	C	GLN	615	36.677	18.478	49.396	1.00	59.82

ATOM	248	O	GLN	615	36.200	19.441	48.784	1.00	60.64
ATOM	249	CB	GLN	615	35.840	16.259	48.801	1.00	62.84
ATOM	250	CG	GLN	615	35.738	15.162	47.795	1.00	62.14
ATOM	251	CD	GLN	615	34.290	14.775	47.573	1.00	58.76
ATOM	252	OE1	GLN	615	33.532	14.598	48.525	1.00	62.70
ATOM	253	NE2	GLN	615	33.897	14.651	46.314	1.00	61.03
TER	254		GLN	615					
ATOM	255	N	PRO	625	30.130	9.828	47.355	1.00	62.43
ATOM	256	CA	PRO	625	29.795	11.035	46.593	1.00	59.45
ATOM	257	C	PRO	625	28.366	11.397	46.928	1.00	62.94
ATOM	258	O	PRO	625	28.111	12.382	47.622	1.00	59.36
ATOM	259	CB	PRO	625	29.949	10.582	45.146	1.00	62.18
ATOM	260	CG	PRO	625	31.089	9.653	45.245	1.00	59.91
ATOM	261	CD	PRO	625	30.706	8.811	46.459	1.00	62.52
TER	262		PRO	625					
ATOM	263	N	TYR	663	50.007	8.771	51.436	1.00	61.62
ATOM	264	CA	TYR	663	48.716	8.186	51.812	1.00	62.54
ATOM	265	C	TYR	663	48.565	6.680	51.537	1.00	59.94
ATOM	266	O	TYR	663	48.090	5.918	52.389	1.00	60.92
ATOM	267	CB	TYR	663	47.601	8.921	51.068	1.00	63.89
ATOM	268	CG	TYR	663	46.266	8.230	51.167	1.00	61.84
ATOM	269	CD1	TYR	663	45.619	8.109	52.392	1.00	59.60
ATOM	270	CD2	TYR	663	45.659	7.676	50.043	1.00	58.65
ATOM	271	CE1	TYR	663	44.407	7.458	52.498	1.00	58.52
ATOM	272	CE2	TYR	663	44.441	7.019	50.138	1.00	60.83
ATOM	273	CZ	TYR	663	43.820	6.916	51.368	1.00	62.58
ATOM	274	OH	TYR	663	42.601	6.287	51.477	1.00	61.21
ATOM	275	N	LEU	664	48.930	6.274	50.325	1.00	60.84
ATOM	276	CA	LEU	664	48.846	4.881	49.908	1.00	61.56
ATOM	277	C	LEU	664	49.744	4.001	50.777	1.00	60.21
ATOM	278	O	LEU	664	49.369	2.889	51.161	1.00	61.89
ATOM	279	CB	LEU	664	49.261	4.757	48.438	1.00	60.37
ATOM	280	CG	LEU	664	48.363	5.402	47.382	1.00	64.33
ATOM	281	CD1	LEU	664	49.036	5.350	46.023	1.00	64.49
ATOM	282	CD2	LEU	664	47.032	4.687	47.351	1.00	59.02
TER	283		LEU	664					
ATOM	284	N	LYS	667	48.446	3.950	54.421	1.00	58.08
ATOM	285	CA	LYS	667	47.241	3.129	54.482	1.00	61.17
ATOM	286	C	LYS	667	47.592	1.658	54.468	1.00	63.84
ATOM	287	O	LYS	667	46.867	0.838	55.011	1.00	61.95

ATOM	288	CB	LYS	667	46.318	3.429	53.305	1.00	66.33
ATOM	289	CG	LYS	667	45.013	2.663	53.338	1.00	59.73
ATOM	290	CD	LYS	667	43.951	3.382	52.532	1.00	60.07
ATOM	291	CE	LYS	667	44.313	3.462	51.063	1.00	62.82
ATOM	292	NZ	LYS	667	44.134	2.158	50.390	1.00	62.44
TER	293		LYS	667					

Example 24

X-ray Structure Coordinates of GR Site II, Table V

Below is Table V, which gives the x-ray structure coordinates for GR Site II discerned from the disclosure in Kauppi et. al., in the Journal of Biological Chemistry Online, JBC Papers In Press as doi:10.1074/jbc.M212711200, April 9, 2003, RCSB file: 1nhz.pdb (GR LBD bound to an antagonist, RU 486). The format used is based on that commonly used in the RCSB (Research Collaboratory for Structural Bioinformatics, pdb file format), and the fields listed from left to right are defined as follows: record name, atom serial number, atom name, residue name, chain identifier, residue sequence number, orthogonal coordinate for x in Ångstroms, orthogonal cordinate for y in Ångstroms, orthogonal coordinate for z in Ångstroms, occupancy, and temperature factor.

Table V

ATOM	1	N	GLU	537	26.949	4.045	83.095	1.00	0.00
ATOM	2	CA	GLU	537	25.828	3.147	82.817	1.00	0.00
ATOM	3	C	GLU	537	24.510	3.903	82.903	1.00	0.00
ATOM	4	O	GLU	537	23.672	3.737	82.043	1.00	0.00
ATOM	5	CB	GLU	537	25.781	1.935	83.756	1.00	0.00
ATOM	6	CG	GLU	537	24.445	1.183	83.643	1.00	0.00
ATOM	7	CD	GLU	537	24.470	-0.233	84.168	1.00	0.00
ATOM	8	OE1	GLU	537	25.374	-0.538	84.996	1.00	0.00
ATOM	9	OE2	GLU	537	23.565	-1.032	83.762	1.00	0.00
ATOM	10	N	VAL	538	24.336	4.753	83.907	1.00	0.00
ATOM	11	CA	VAL	538	23.045	5.402	84.089	1.00	0.00
ATOM	12	C	VAL	538	22.743	6.413	82.968	1.00	0.00
ATOM	13	O	VAL	538	21.598	6.534	82.552	1.00	0.00

ATOM	14	CB	VAL	538	22.824	6.035	85.527	1.00	0.00
ATOM	15	CG1	VAL	538	23.344	5.107	86.654	1.00	0.00
ATOM	16	CG2	VAL	538	23.413	7.415	85.654	1.00	0.00
ATOM	17	N	ILE	539	23.742	7.119	82.470	1.00	0.00
ATOM	18	CA	ILE	539	23.496	8.120	81.427	1.00	0.00
ATOM	19	C	ILE	539	23.537	7.549	79.994	1.00	0.00
ATOM	20	O	ILE	539	23.320	8.285	79.043	1.00	0.00
ATOM	21	CB	ILE	539	24.471	9.322	81.550	1.00	0.00
ATOM	22	CG1	ILE	539	25.908	8.862	81.348	1.00	0.00
ATOM	23	CG2	ILE	539	24.329	10.017	82.914	1.00	0.00
ATOM	24	CD1	ILE	539	26.805	9.907	80.746	1.00	0.00
ATOM	25	N	GLU	540	23.820	6.263	79.846	1.00	0.00
ATOM	26	CA	GLU	540	23.875	5.614	78.522	1.00	0.00
ATOM	27	C	GLU	540	22.497	5.764	77.805	1.00	0.00
ATOM	28	O	GLU	540	21.463	5.478	78.377	1.00	0.00
ATOM	29	CB	GLU	540	24.313	4.129	78.698	1.00	0.00
ATOM	30	CG	GLU	540	24.605	3.310	77.424	1.00	0.00
ATOM	31	CD	GLU	540	25.530	3.964	76.393	1.00	0.00
ATOM	32	OE1	GLU	540	25.387	3.568	75.196	1.00	0.00
ATOM	33	OE2	GLU	540	26.383	4.837	76.748	1.00	0.00
ATOM	34	N	PRO	541	22.480	6.288	76.578	1.00	0.00
ATOM	35	CA	PRO	541	21.219	6.557	75.887	1.00	0.00
ATOM	36	C	PRO	541	20.356	5.307	75.680	1.00	0.00
ATOM	37	O	PRO	541	20.873	4.266	75.401	1.00	0.00
ATOM	38	CB	PRO	541	21.683	7.067	74.527	1.00	0.00
ATOM	39	CG	PRO	541	23.067	7.581	74.749	1.00	0.00
ATOM	40	CD	PRO	541	23.639	6.678	75.759	1.00	0.00
ATOM	41	N	GLU	542	19.049	5.419	75.801	1.00	0.00
ATOM	42	CA	GLU	542	18.163	4.373	75.290	1.00	0.00
ATOM	43	C	GLU	542	18.327	4.201	73.782	1.00	0.00
ATOM	44	O	GLU	542	18.747	5.141	73.056	1.00	0.00
ATOM	45	CB	GLU	542	16.706	4.701	75.586	1.00	0.00
ATOM	46	CG	GLU	542	16.392	4.783	77.062	1.00	0.00
ATOM	47	CD	GLU	542	14.923	5.041	77.333	1.00	0.00
ATOM	48	OE1	GLU	542	14.131	5.127	76.358	1.00	0.00
ATOM	49	OE2	GLU	542	14.565	5.168	78.522	1.00	0.00
ATOM	50	N	VAL	543	18.014	2.994	73.322	1.00	0.00
ATOM	51	CA	VAL	543	18.041	2.659	71.904	1.00	0.00
ATOM	52	C	VAL	543	16.769	3.187	71.221	1.00	0.00
ATOM	53	O	VAL	543	15.652	2.913	71.645	1.00	0.00

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ATOM     54  CB  VAL   543      18.231   1.127  71.699  1.00  0.00
ATOM     55  CG1 VAL   543      17.014   0.387  72.184  1.00  0.00
ATOM     56  CG2 VAL   543      18.414   0.803  70.241  1.00  0.00
TER      57      VAL   543
ATOM     58  N   LEU   566      17.090   9.013  61.502  1.00  0.00
ATOM     59  CA  LEU   566      17.579   8.376  62.706  1.00  0.00
ATOM     60  C   LEU   566      18.952   8.946  63.111  1.00  0.00
ATOM     61  O   LEU   566      19.208   9.149  64.289  1.00  0.00
ATOM     62  CB  LEU   566      17.630   6.849  62.519  1.00  0.00
ATOM     63  CG  LEU   566      18.276   6.057  63.667  1.00  0.00
ATOM     64  CD1 LEU   566      17.436   6.181  64.939  1.00  0.00
ATOM     65  CD2 LEU   566      18.455   4.644  63.275  1.00  0.00
ATOM     66  N   GLY   567      19.844   9.183  62.155  1.00  0.00
ATOM     67  CA  GLY   567      21.173   9.724  62.456  1.00  0.00
ATOM     68  C   GLY   567      21.184  11.113  63.098  1.00  0.00
ATOM     69  O   GLY   567      21.956  11.389  64.033  1.00  0.00
TER      70      GLY   567
ATOM     71  N   GLN   570      20.184  10.552  66.664  1.00  0.00
ATOM     72  CA  GLN   570      21.237   9.937  67.467  1.00  0.00
ATOM     73  C   GLN   570      22.303  10.951  67.864  1.00  0.00
ATOM     74  O   GLN   570      22.800  10.900  68.978  1.00  0.00
ATOM     75  CB  GLN   570      21.888   8.769  66.721  1.00  0.00
ATOM     76  CG  GLN   570      21.014   7.523  66.606  1.00  0.00
ATOM     77  CD  GLN   570      21.775   6.239  66.219  1.00  0.00
ATOM     78  OE1 GLN   570      21.183   5.150  66.188  1.00  0.00
ATOM     79  NE2 GLN   570      23.046   6.353  65.935  1.00  0.00
ATOM     80  N   VAL   571      22.632  11.873  66.948  1.00  0.00
ATOM     81  CA  VAL   571      23.474  13.031  67.233  1.00  0.00
ATOM     82  C   VAL   571      22.909  13.850  68.390  1.00  0.00
ATOM     83  O   VAL   571      23.632  14.163  69.310  1.00  0.00
ATOM     84  CB  VAL   571      23.685  13.922  65.994  1.00  0.00
ATOM     85  CG1 VAL   571      24.439  15.225  66.326  1.00  0.00
ATOM     86  CG2 VAL   571      24.492  13.214  64.979  1.00  0.00
ATOM     87  N   ILE   572      21.622  14.175  68.366  1.00  0.00
ATOM     88  CA  ILE   572      21.011  14.888  69.472  1.00  0.00
ATOM     89  C   ILE   572      21.175  14.114  70.772  1.00  0.00
ATOM     90  O   ILE   572      21.438  14.708  71.803  1.00  0.00
ATOM     91  CB  ILE   572      19.511  15.163  69.238  1.00  0.00
ATOM     92  CG1 ILE   572      19.267  16.067  68.031  1.00  0.00
ATOM     93  CG2 ILE   572      18.825  15.804  70.530  1.00  0.00
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ATOM	94	CD1	ILE	572	20.291	17.128	67.843	1.00	0.00
ATOM	95	N	ALA	573	21.006	12.800	70.727	1.00	0.00
ATOM	96	CA	ALA	573	21.188	11.972	71.920	1.00	0.00
ATOM	97	C	ALA	573	22.683	11.844	72.355	1.00	0.00
ATOM	98	O	ALA	573	22.946	11.714	73.538	1.00	0.00
ATOM	99	CB	ALA	573	20.555	10.598	71.713	1.00	0.00
ATOM	100	N	ALA	574	23.629	11.873	71.416	1.00	0.00
ATOM	101	CA	ALA	574	25.057	11.920	71.732	1.00	0.00
ATOM	102	C	ALA	574	25.470	13.202	72.483	1.00	0.00
ATOM	103	O	ALA	574	26.280	13.158	73.394	1.00	0.00
ATOM	104	CB	ALA	574	25.887	11.795	70.468	1.00	0.00
ATOM	105	N	VAL	575	24.897	14.339	72.085	1.00	0.00
ATOM	106	CA	VAL	575	25.196	15.612	72.722	1.00	0.00
ATOM	107	C	VAL	575	24.679	15.597	74.137	1.00	0.00
ATOM	108	O	VAL	575	25.403	15.925	75.107	1.00	0.00
ATOM	109	CB	VAL	575	24.568	16.781	71.924	1.00	0.00
ATOM	110	CG1	VAL	575	24.768	18.084	72.645	1.00	0.00
ATOM	111	CG2	VAL	575	25.179	16.813	70.517	1.00	0.00
ATOM	112	N	LYS	576	23.443	15.142	74.281	1.00	0.00
ATOM	113	CA	LYS	576	22.833	15.038	75.596	1.00	0.00
ATOM	114	C	LYS	576	23.602	14.088	76.541	1.00	0.00
ATOM	115	O	LYS	576	23.770	14.370	77.733	1.00	0.00
ATOM	116	CB	LYS	576	21.339	14.722	75.422	1.00	0.00
ATOM	117	CG	LYS	576	20.637	13.971	76.547	1.00	0.00
ATOM	118	CD	LYS	576	20.466	14.768	77.796	1.00	0.00
ATOM	119	CE	LYS	576	19.157	14.388	78.557	1.00	0.00
ATOM	120	NZ	LYS	576	18.232	13.432	77.808	1.00	0.00
ATOM	121	N	TRP	577	24.091	12.987	76.012	1.00	0.00
ATOM	122	CA	TRP	577	24.939	12.051	76.760	1.00	0.00
ATOM	123	C	TRP	577	26.259	12.737	77.181	1.00	0.00
ATOM	124	O	TRP	577	26.604	12.777	78.340	1.00	0.00
ATOM	125	CB	TRP	577	25.224	10.833	75.872	1.00	0.00
ATOM	126	CG	TRP	577	26.324	9.975	76.319	1.00	0.00
ATOM	127	CD1	TRP	577	26.276	9.030	77.295	1.00	0.00
ATOM	128	CD2	TRP	577	27.639	9.915	75.762	1.00	0.00
ATOM	129	NE1	TRP	577	27.494	8.424	77.423	1.00	0.00
ATOM	130	CE2	TRP	577	28.351	8.943	76.481	1.00	0.00
ATOM	131	CE3	TRP	577	28.297	10.604	74.730	1.00	0.00
ATOM	132	CZ2	TRP	577	29.683	8.650	76.217	1.00	0.00
ATOM	133	CZ3	TRP	577	29.600	10.333	74.488	1.00	0.00

	ATOM	134	CH2	TRP	577	30.285	9.354	75.207	1.00	0.00
	TER	135		TRP	577					
	ATOM	136	N	SER	599	33.944	13.837	67.076	1.00	0.00
	ATOM	137	CA	SER	599	33.791	12.478	67.530	1.00	0.00
	ATOM	138	C	SER	599	32.416	11.902	67.351	1.00	0.00
	ATOM	139	O	SER	599	32.274	10.694	67.529	1.00	0.00
	ATOM	140	CB	SER	599	34.200	12.381	69.007	1.00	0.00
	ATOM	141	OG	SER	599	33.158	12.943	69.797	1.00	0.00
	ATOM	142	N	TRP	600	31.417	12.686	66.954	1.00	0.00
	ATOM	143	CA	TRP	600	30.053	12.122	66.862	1.00	0.00
	ATOM	144	C	TRP	600	29.906	10.885	65.951	1.00	0.00
	ATOM	145	O	TRP	600	29.176	9.955	66.262	1.00	0.00
	ATOM	146	CB	TRP	600	28.985	13.176	66.533	1.00	0.00
	ATOM	147	CG	TRP	600	29.029	13.741	65.176	1.00	0.00
	ATOM	148	CD1	TRP	600	29.530	14.957	64.832	1.00	0.00
	ATOM	149	CD2	TRP	600	28.521	13.159	63.961	1.00	0.00
	ATOM	150	NE1	TRP	600	29.378	15.168	63.488	1.00	0.00
	ATOM	151	CE2	TRP	600	28.761	14.084	62.923	1.00	0.00
	ATOM	152	CE3	TRP	600	27.875	11.962	63.644	1.00	0.00
	ATOM	153	CZ2	TRP	600	28.389	13.842	61.584	1.00	0.00
	ATOM	154	CZ3	TRP	600	27.507	11.713	62.310	1.00	0.00
	ATOM	155	CH2	TRP	600	27.748	12.648	61.307	1.00	0.00
	ATOM	156	N	MET	601	30.634	10.843	64.848	1.00	0.00
	ATOM	157	CA	MET	601	30.494	9.691	63.964	1.00	0.00
	ATOM	158	C	MET	601	31.122	8.461	64.655	1.00	0.00
	ATOM	159	O	MET	601	30.582	7.387	64.607	1.00	0.00
	ATOM	160	CB	MET	601	31.142	9.953	62.620	1.00	0.00
	ATOM	161	CG	MET	601	31.047	8.813	61.588	1.00	0.00
	ATOM	162	SD	MET	601	29.324	8.553	60.991	1.00	0.00
	ATOM	163	CE	MET	601	29.347	9.653	59.543	1.00	0.00
	ATOM	164	N	SER	602	32.284	8.637	65.271	1.00	0.00
	ATOM	165	CA	SER	602	32.954	7.575	65.985	1.00	0.00
	ATOM	166	C	SER	602	32.055	6.975	67.064	1.00	0.00
	ATOM	167	O	SER	602	31.966	5.774	67.198	1.00	0.00
	ATOM	168	CB	SER	602	34.224	8.119	66.622	1.00	0.00
	ATOM	169	OG	SER	602	35.066	7.041	66.994	1.00	0.00
	ATOM	170	N	LEU	603	31.383	7.822	67.825	1.00	0.00
	ATOM	171	CA	LEU	603	30.530	7.383	68.933	1.00	0.00
	ATOM	172	C	LEU	603	29.331	6.614	68.450	1.00	0.00
	ATOM	173	O	LEU	603	28.976	5.602	69.021	1.00	0.00

	ATOM	174	CB	LEU	603	30.008	8.560	69.746	1.00	0.00
	ATOM	175	CG	LEU	603	31.053	9.411	70.448	1.00	0.00
	ATOM	176	CD1	LEU	603	30.409	10.692	70.907	1.00	0.00
	ATOM	177	CD2	LEU	603	31.573	8.704	71.615	1.00	0.00
5	ATOM	178	N	MET	604	28.716	7.098	67.385	1.00	0.00
	ATOM	179	CA	MET	604	27.565	6.405	66.803	1.00	0.00
	ATOM	180	C	MET	604	27.914	5.076	66.137	1.00	0.00
	ATOM	181	O	MET	604	27.150	4.114	66.248	1.00	0.00
	ATOM	182	CB	MET	604	26.834	7.333	65.826	1.00	0.00
10	ATOM	183	CG	MET	604	26.029	8.373	66.615	1.00	0.00
	ATOM	184	SD	MET	604	25.459	9.825	65.626	1.00	0.00
	ATOM	185	CE	MET	604	24.810	8.937	64.246	1.00	0.00
	ATOM	186	N	ALA	605	29.062	5.018	65.465	1.00	0.00
	ATOM	187	CA	ALA	605	29.507	3.760	64.823	1.00	0.00
15	ATOM	188	C	ALA	605	29.891	2.728	65.897	1.00	0.00
	ATOM	189	O	ALA	605	29.656	1.535	65.720	1.00	0.00
	ATOM	190	CB	ALA	605	30.712	4.035	63.882	1.00	0.00
	ATOM	191	N	PHE	606	30.454	3.204	67.028	1.00	0.00
	ATOM	192	CA	PHE	606	30.868	2.345	68.135	1.00	0.00
20	ATOM	193	C	PHE	606	29.663	1.746	68.854	1.00	0.00
	ATOM	194	O	PHE	606	29.642	0.569	69.130	1.00	0.00
	ATOM	195	CB	PHE	606	31.741	3.102	69.128	1.00	0.00
	ATOM	196	CG	PHE	606	32.577	2.209	69.997	1.00	0.00
	ATOM	197	CD1	PHE	606	33.528	1.379	69.442	1.00	0.00
25	ATOM	198	CD2	PHE	606	32.423	2.207	71.378	1.00	0.00
	ATOM	199	CE1	PHE	606	34.303	0.556	70.248	1.00	0.00
	ATOM	200	CE2	PHE	606	33.195	1.399	72.194	1.00	0.00
	ATOM	201	CZ	PHE	606	34.132	0.569	71.648	1.00	0.00
	ATOM	202	N	ALA	607	28.655	2.552	69.116	1.00	0.00
30	ATOM	203	CA	ALA	607	27.432	2.068	69.751	1.00	0.00
	ATOM	204	C	ALA	607	26.656	1.180	68.791	1.00	0.00
	ATOM	205	O	ALA	607	26.075	0.162	69.213	1.00	0.00
	ATOM	206	CB	ALA	607	26.606	3.233	70.199	1.00	0.00
	TER	207		ALA	607					
35	ATOM	208	N	TRP	610	28.346	-2.104	69.065	1.00	0.00
	ATOM	209	CA	TRP	610	27.953	-2.735	70.319	1.00	0.00
	ATOM	210	C	TRP	610	26.577	-3.372	70.237	1.00	0.00
	ATOM	211	O	TRP	610	26.421	-4.534	70.610	1.00	0.00
	ATOM	212	CB	TRP	610	28.040	-1.731	71.469	1.00	0.00
40	ATOM	213	CG	TRP	610	27.584	-2.314	72.758	1.00	0.00

```
ATOM    214  CD1 TRP   610      26.347  -2.161  73.356  1.00  0.00
ATOM    215  CD2 TRP   610      28.334  -3.183  73.609  1.00  0.00
ATOM    216  NE1 TRP   610      26.310  -2.864  74.532  1.00  0.00
ATOM    217  CE2 TRP   610      27.507  -3.517  74.704  1.00  0.00
ATOM    218  CE3 TRP   610      29.630  -3.712  73.564  1.00  0.00
ATOM    219  CZ2 TRP   610      27.935  -4.341  75.732  1.00  0.00
ATOM    220  CZ3 TRP   610      30.040  -4.541  74.584  1.00  0.00
ATOM    221  CH2 TRP   610      29.202  -4.842  75.652  1.00  0.00
ATOM    222  N   ARG   611      25.611  -2.643  69.698  1.00  0.00
ATOM    223  CA  ARG   611      24.296  -3.167  69.471  1.00  0.00
ATOM    224  C   ARG   611      24.337  -4.398  68.582  1.00  0.00
ATOM    225  O   ARG   611      23.635  -5.363  68.865  1.00  0.00
ATOM    226  CB  ARG   611      23.350  -2.102  68.853  1.00  0.00
ATOM    227  CG  ARG   611      22.907  -1.050  69.843  1.00  0.00
ATOM    228  CD  ARG   611      21.755  -0.166  69.401  1.00  0.00
ATOM    229  NE  ARG   611      21.899   0.318  68.043  1.00  0.00
ATOM    230  CZ  ARG   611      22.496   1.444  67.662  1.00  0.00
ATOM    231  NH1 ARG   611      23.083   2.262  68.503  1.00  0.00
ATOM    232  NH2 ARG   611      22.551   1.737  66.376  1.00  0.00
TER     233       ARG   611
ATOM    234  N   ARG   614      25.776  -7.384  70.378  1.00  0.00
ATOM    235  CA  ARG   614      24.958  -7.840  71.479  1.00  0.00
ATOM    236  C   ARG   614      23.643  -8.468  71.041  1.00  0.00
ATOM    237  O   ARG   614      23.239  -9.504  71.557  1.00  0.00
ATOM    238  CB  ARG   614      24.681  -6.657  72.407  1.00  0.00
ATOM    239  CG  ARG   614      24.963  -6.918  73.839  1.00  0.00
ATOM    240  CD  ARG   614      26.436  -7.104  74.156  1.00  0.00
ATOM    241  NE  ARG   614      26.731  -8.517  74.370  1.00  0.00
ATOM    242  CZ  ARG   614      27.372  -9.045  75.417  1.00  0.00
ATOM    243  NH1 ARG   614      27.791  -8.303  76.446  1.00  0.00
ATOM    244  NH2 ARG   614      27.608 -10.351  75.425  1.00  0.00
ATOM    245  N   GLN   615      22.973  -7.828  70.100  1.00  0.00
ATOM    246  CA  GLN   615      21.685  -8.299  69.591  1.00  0.00
ATOM    247  C   GLN   615      21.782  -9.480  68.626  1.00  0.00
ATOM    248  O   GLN   615      20.869 -10.301  68.601  1.00  0.00
ATOM    249  CB  GLN   615      20.942  -7.142  68.923  1.00  0.00
ATOM    250  CG  GLN   615      20.559  -6.039  69.902  1.00  0.00
ATOM    251  CD  GLN   615      19.647  -6.546  70.990  1.00  0.00
ATOM    252  OE1 GLN   615      18.595  -7.114  70.687  1.00  0.00
ATOM    253  NE2 GLN   615      20.066  -6.416  72.251  1.00  0.00
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TER	254		GLN	615					
ATOM	255	N	PRO	625	16.074	-1.390	66.522	1.00	0.00
ATOM	256	CA	PRO	625	15.326	-2.645	66.670	1.00	0.00
ATOM	257	C	PRO	625	14.446	-2.972	65.466	1.00	0.00
ATOM	258	O	PRO	625	14.219	-4.123	65.155	1.00	0.00
ATOM	259	CB	PRO	625	14.451	-2.387	67.917	1.00	0.00
ATOM	260	CG	PRO	625	15.230	-1.373	68.700	1.00	0.00
ATOM	261	CD	PRO	625	15.816	-0.460	67.630	1.00	0.00
TER	262		PRO	625					
ATOM	263	N	TYR	663	33.300	-1.331	77.384	1.00	0.00
ATOM	264	CA	TYR	663	32.605	-0.587	76.345	1.00	0.00
ATOM	265	C	TYR	663	32.220	0.825	76.775	1.00	0.00
ATOM	266	O	TYR	663	32.422	1.772	76.039	1.00	0.00
ATOM	267	CB	TYR	663	31.366	-1.372	75.911	1.00	0.00
ATOM	268	CG	TYR	663	30.348	-0.537	75.200	1.00	0.00
ATOM	269	CD1	TYR	663	30.558	-0.163	73.888	1.00	0.00
ATOM	270	CD2	TYR	663	29.164	-0.139	75.821	1.00	0.00
ATOM	271	CE1	TYR	663	29.632	0.607	73.206	1.00	0.00
ATOM	272	CE2	TYR	663	28.221	0.647	75.125	1.00	0.00
ATOM	273	CZ	TYR	663	28.493	1.012	73.822	1.00	0.00
ATOM	274	OH	TYR	663	27.616	1.758	73.058	1.00	0.00
ATOM	275	N	LEU	664	31.685	0.992	77.971	1.00	0.00
ATOM	276	CA	LEU	664	31.341	2.335	78.447	1.00	0.00
ATOM	277	C	LEU	664	32.559	3.273	78.520	1.00	0.00
ATOM	278	O	LEU	664	32.478	4.449	78.147	1.00	0.00
ATOM	279	CB	LEU	664	30.682	2.262	79.818	1.00	0.00
ATOM	280	CG	LEU	664	29.314	1.540	79.897	1.00	0.00
ATOM	281	CD1	LEU	664	28.821	1.419	81.337	1.00	0.00
ATOM	282	CD2	LEU	664	28.309	2.263	79.064	1.00	0.00
TER	283		LEU	664					
ATOM	284	N	LYS	667	33.939	4.070	75.029	1.00	0.00
ATOM	285	CA	LYS	667	33.100	5.011	74.302	1.00	0.00
ATOM	286	C	LYS	667	33.330	6.463	74.740	1.00	0.00
ATOM	287	O	LYS	667	33.376	7.376	73.914	1.00	0.00
ATOM	288	CB	LYS	667	31.622	4.597	74.408	1.00	0.00
ATOM	289	CG	LYS	667	30.709	5.423	73.574	1.00	0.00
ATOM	290	CD	LYS	667	29.419	4.683	73.210	1.00	0.00
ATOM	291	CE	LYS	667	28.426	4.543	74.330	1.00	0.00
ATOM	292	NZ	LYS	667	28.369	5.641	75.303	1.00	0.00
TER	293		LYS	667					

What is claimed is:

1. A method for evaluating the potential of a chemical entity to bind to all or any part of Site II comprising:
   (a) docking a chemical entity into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; and
   (b) analyzing structural and chemical feature complementarity between said chemical entity and all or any part of said Site II.
2. The method of claim 1, wherein the Site II is an NHR Site II.
3. The method of claim 1, wherein the Site II is an SHR Site II.
4. The method of claim 1, wherein the Site II is a GR Site II.
5. A method of designing a ligand of Site II comprising:
   (a) modeling all or any part of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I; and
   (b) based on said modeling, designing a chemical entity that has structural and chemical feature complementarity with all or any part of said Site II.
6. A method for identifying a modulator of an NHR comprising:
   (a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566,

G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I;

(b) analyzing structural and chemical feature complementarity between the test molecule and all or any part said Site II; and

(c) screening the test molecule in a biological assay of modulation of an NHR.

7. The method of claim 6 further comprising one or more of the following:

(d) screening the test molecule in an assay that characterizes binding to a Site II; and

(e) screening the test molecule in an assay that characterizes binding to Site I.

8. The method of claim 6, wherein the modulator of an NHR induces transrepression.

9. The method of claim 6, wherein the modulator of an NHR is a dissociated compound.

10. The method of claim 6, wherein the modulator of an NHR antagonizes a modulator that induces transactivation.

11. The method of claim 9, wherein the dissociated compound is an SHR dissociated compound.

12. The method of claim 11, wherein the SHR dissociated compound is a GR dissociated compound.

13. The method of claim 6, wherein the Site II is an NHR Site II selected from the Site IIs of the group consisting of: RXR-alpha; RXR-beta; progesterone receptor (PR); androgen receptor (AR); estrogen receptor-alpha (ER-alpha); ER-beta; vitamin D receptor (VitDR); peroxisome proliferator activated receptor-gamma (PPAR-gamma); thyroid receptor-alpha (TR-alpha); TR-beta; mineralocorticoid receptor (MR); and glucocorticoid receptor (GR).

14. The method of claim 13, wherein the NHR Site II is an SHR Site II selected from the Site IIs of the group consisting of: PR; AR; ER-alpha; ER-beta; MR; and GR.

15. The method of claim 14, wherein said SHR Site II is a GR Site II.

16. The method of claim 15, wherein the GR Site II is selected from the Site IIs of the group consisting of: human GR; rat GR; mouse GR; sheep GR; marmoset GR; squirrel GR; pig GR; guinea pig GR; and m'az monkey GR.

17. The method of claim 13, wherein the NHR Site II is a RXR-alpha Site II composed of amino acids L236-P244, A272-A273, Q276-W283, G305-S313, H316-R317, A320-V321, T329, L368-G369, and R372 according to Figure 2.

18. The method of claim 13, wherein the the NHR Site II is a RAR-gamma Site II composed of amino acids S194-P202, L233-A234, C237-F244, A266-R274, T277-R278, T280-E282, D290, T328-G329 and S332 according to Figure 2.

19. The method of claim 13, wherein the the NHR Site II is a PR Site II composed of amino acids M692-V698, L721-G722, Q725-W732, S754-G762, W765-R766, K769-H770, P780, F818-L819 and K822 according to Figure 2.

20. The method of claim 13, wherein the the NHR Site II is a AR Site II composed of amino acids E678-V684, L708-G709, Q712-W719, S741-A749, W752-R753, T756-N757, P767, F805-L806 and K809 according to Figure 2.

21. The method of claim 13, wherein the the NHR Site II is a ER-alpha Site II composed of amino acids L320-I326, L348-A349, E352-W359, A381, W382-G389, W392-R393, E396, P405, F444-V445 and K448 according to Figure 2.

22. The method of claim 13, wherein the the NHR Site II is a ER-beta Site II composed of amino acids L273-H279, L297-A298, E301-W308, C330-G338, W341-R342, D345, P354, Y393-L394 and K397 according to Figure 2.

23. The method of claim 13, wherein the the NHR Site II is a VitDR Site II composed of amino acids L136-D144, L182-V183, S186-F193, S215-R223, E226-S227, T229-D231, G238, H279-V280 and M283 according to Figure 2.

24. The method of claim 13, wherein the the NHR Site II is a PPAR-gamma Site II composed of amino acids Y219-P227, R288-S289, A292-Y299, G321-M329, S332-L333, N335-K336, E343, L384-A385 and I388 according to Figure 2.

25. The method of claim 13, wherein the the NHR Site II is a MR Site II composed of amino acids E743-I749, L772-A773, Q776-W783, S805-A813, W816-R817, K820-H821, P831, Y869-T870 and K873 according to Figure 2.

26. The method of claim 13, wherein the the NHR Site II is a TR-beta Site II composed of amino acids T226-Q235, I267-I268, A271-F278, C300-R308, V311-R312, D314-E316, G324, V362-A363 and Q366 according to Figure 2.

27. The method of claim 13, wherein the the NHR Site II is a GR Site II composed of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Figure 2.

28. The method of claim 27, wherein the structure coordinates of the GR Site II define the structure of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I, Table III, Table IV, or Table V.

29. A method for identifying a ligand of Site II comprising:

(a) docking a test molecule into all or any part of the cavity circumscribed by a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I;

(b) analyzing structural and chemical feature complementarity between the test molecule and all or any part said Site II; and

(c) screening the test molecule in an assay that characterizes binding to a Site II.

30. A ligand of a Site II, wherein said Site II is a structure defined by structure coordinates that describe conserved residue backbone atoms having a root mean square deviation of not more than 2.0 Å from the conserved residue backbone atoms described by the structure coordinates of amino acids E537-V543, L566, G567, Q570-W577, S599-A607, W610, R611, R614, Q615, P625, Y663, L664 and K667 according to Table I.

31. A modulator of an NHR, wherein said modulator has been identified by the method of claim 6.

32. A modulator of an NHR that is a ligand of claim 30.

33. A method of modulating an NHR comprising administering a modulator of an NHR in an amount sufficient to modulate the NHR, wherein said modulator of an NHR is a modulator of claim 31.

34. A method of modulating an NHR comprising administering a modulator of an NHR in an amount sufficient to modulate the NHR, wherein said modulator of an NHR is a modulator of claim 32.

35. A method of treating an NHR-associated disease comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR of claim 31.

36. A method of treating an NHR-associated disease comprising administering to a subject in need thereof, in an amount effective therefore, at least one modulator of an NHR of claim 32.

37. A mutant NHR, or a mutant portion of an NHR, comprising one or more amino acid mutations in Site II.

38. A method of measuring the binding of a test molecule to Site II comprising:
(a) incubating an NHR with a ligand of Site II and said test molecule; and
(b) measuring the ability of said test molecule to compete for binding to said Site II with said ligand, wherein said ability to compete is the measure of binding of said test molecule to Site II.

39. The method of claim 38, wherein step (a) further comprises a Site I ligand, wherein the ligand of Site II inhibits the binding of the Site I ligand to Site I, wherein the test molecule does not inhibit the binding of the Site I ligand to Site I, and wherein the measurement of the ability of said test molecule to compete for binding to said Site II is a measurement of the Site I ligand binding to Site I.

FIGURE 1

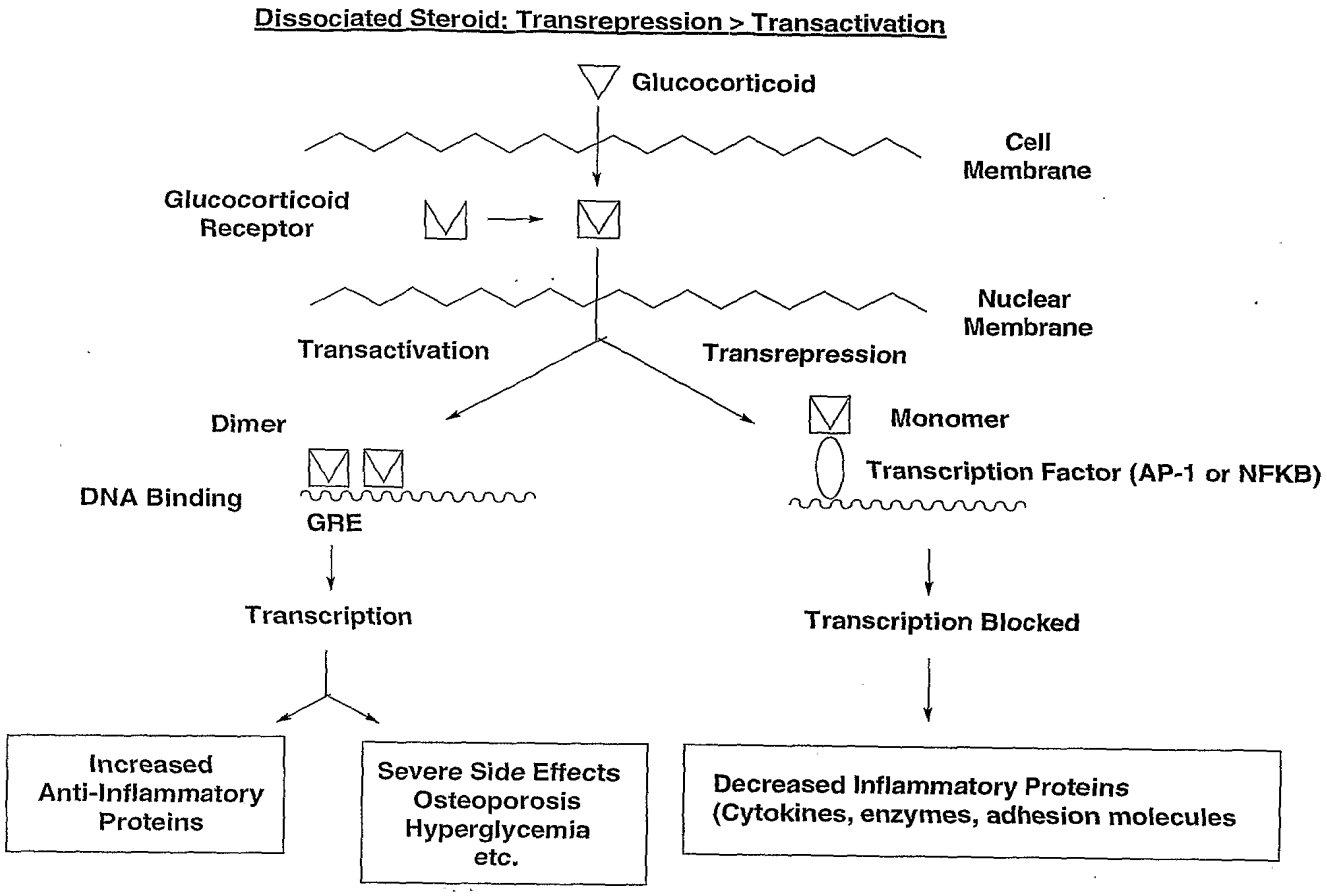

Dissociated Steroid: Transrepression > Transactivation
Glucocorticoid
Cell Membrane
Glucocorticoid Receptor
Nuclear Membrane
Transactivation
Transrepression
Dimer
Monomer
DNA Binding
GRE
Transcription Factor (AP-1 or NFKB)
Transcription
Transcription Blocked
Increased Anti-Inflammatory Proteins
Severe Side Effects Osteoporosis Hyperglycemia etc.
Decreased Inflammatory Proteins (Cytokines, enzymes, adhesion molecules

FIGURE 2

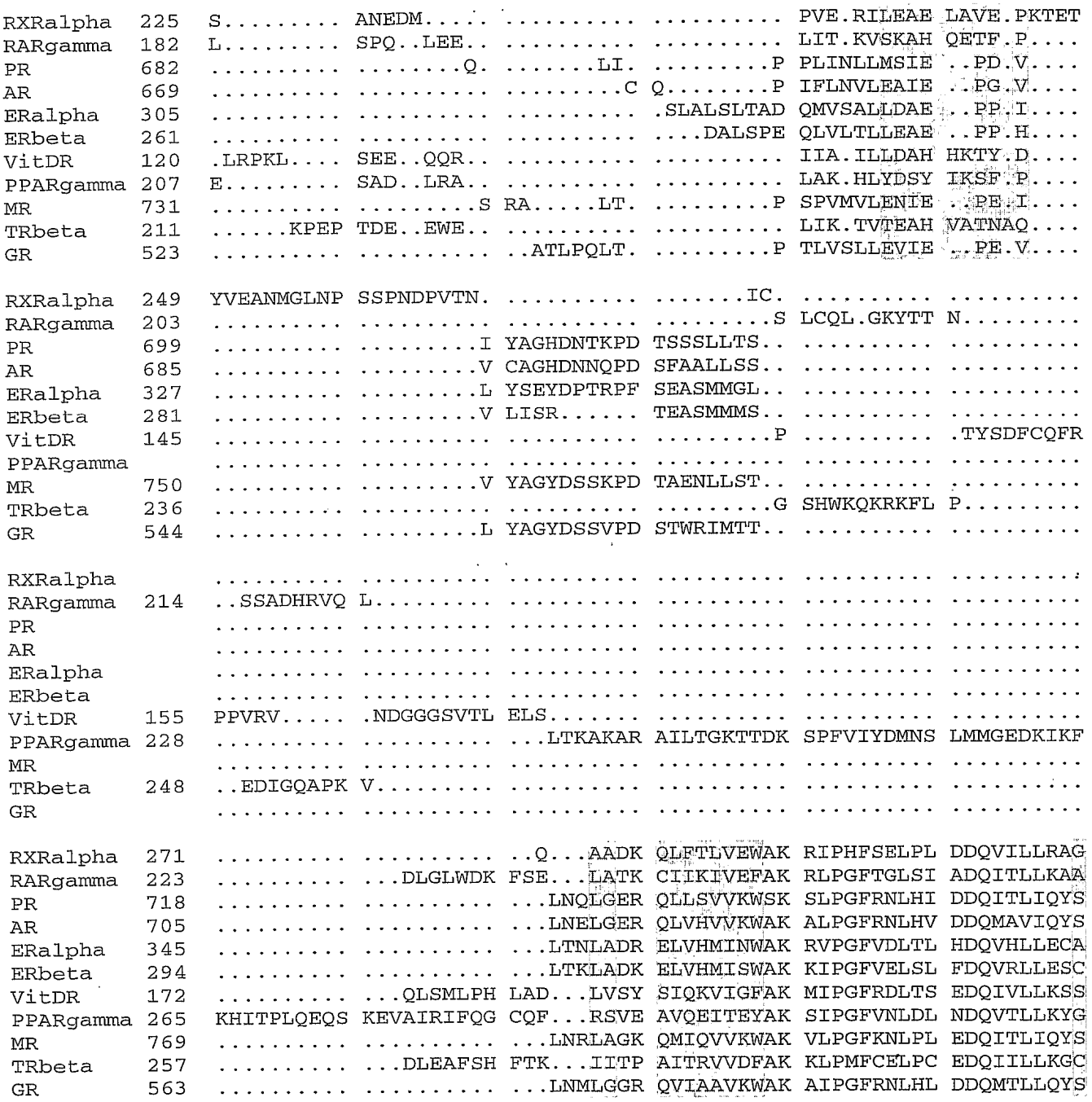

RXRalpha 225 S..... ANEDM..... .... PVE.RILEAE LAVE.PKTET
RARgamma 182 L..... SPQ..LEE.. .... LIT.KVSKAH QETF.P....
PR 682 ....Q. .....LI. .....P PLINLLMSIE ..PD.V....
AR 669 ....C Q.....P IFLNVLEAIE ..PG.V....
ERalpha 305 .... .SLALSLTAD QMVSALLDAE ..PP.I....
ERbeta 261 ....DALSPE QLVLTLLEAE ..PP.H....
VitDR 120 .LRPKL.... SEE..QQR.. .... IIA.ILLDAH HKTY.D....
PPARgamma 207 E..... SAD..LRA.. .... LAK.HLYDSY IKSF.P....
MR 731 ....S RA.....LT. .....P SPVMVLENIE ..PE.I....
TRbeta 211 .....KPEP TDE..EWE.. .... LIK.TVTEAH VATNAQ....
GR 523 ....ATLPQLT. .....P TLVSLLEVIE ..PE.V....
RXRalpha 249 YVEANMGLNP SSPNDPVTN. ....IC. ....
RARgamma 203 ....S LCQL.GKYTT N.....
PR 699 ....I YAGHDNTKPD TSSSLLTS.. ....
AR 685 ....V CAGHDNNQPD SFAALLSS.. ....
ERalpha 327 ....L YSEYDPTRPF SEASMMGL.. ....
ERbeta 281 ....V LISR..... TEASMMMS.. ....
VitDR 145 ....P ..... .TYSDFCQFR
PPARgamma ....
MR 750 ....V YAGYDSSKPD TAENLLST.. ....
TRbeta 236 ....G SHWKQKRKFL P.....
GR 544 ....L YAGYDSSVPD STWRIMTT.. ....
RXRalpha ....
RARgamma 214 ..SSADHRVQ L..... ....
PR ....
AR ....
ERalpha ....
ERbeta ....
VitDR 155 PPVRV..... .NDGGGSVTL ELS..... ....
PPARgamma 228 ....LTKAKAR AILTGKTTDK SPFVIYDMNS LMMGEDKIKF
MR ....
TRbeta 248 ..EDIGQAPK V..... ....
GR ....
RXRalpha 271 ....Q...AADK QLFTLVEWAK RIPHFSELPL DDQVILLRAG
RARgamma 223 ....DLGLWDK FSE...LATK CIIKIVEFAK RLPGFTGLSI ADQITLLKAA
PR 718 ....LNQLGER QLLSVVKWSK SLPGFRNLHI DDQITLIQYS
AR 705 ....LNELGER QLVHVVKWAK ALPGFRNLHV DDQMAVIQYS
ERalpha 345 ....LTNLADR ELVHMINWAK RVPGFVDLTL HDQVHLLECA
ERbeta 294 ....LTKLADK ELVHMISWAK KIPGFVELSL FDQVRLLESC
VitDR 172 ....QLSMLPH LAD...LVSY SIQKVIGFAK MIPGFRDLTS EDQIVLLKSS
PPARgamma 265 KHITPLQEQS KEVAIRIFQG CQF...RSVE AVQEITEYAK SIPGFVNLDL NDQVTLLKYG
MR 769 ....LNRLAGK QMIQVVKWAK VLPGFKNLPL EDQITLIQYS
TRbeta 257 ....DLEAFSH FTK...IITP AITRVVDFAK KLPMFCELPC EDQIILLKGC
GR 563 ....LNMLGGR QVIAAVKWAK AIPGFRNLHL DDQMTLLQYS

FIGURE 2 (continued)

```
RXRalpha      306  WNELLIASFS HRSIAV....  ..KDGILLAT GL...HVHRN ..S..AHSAG VG........
RARgamma      267  CLDILMLRIC TRY...TPE.  ..QDTMTFSD GL...TLNRT ..Q..MH...  ..NAGF....
PR            755  WMSLMVFGLG WRSYK....H VSGQMLYFAP DL...ILNEQ ..R..MKESS FY........
AR            742  WMGLMVFAMG WRSFT....N VNSRMLYFAP DL...VFNEY ..RM.HKSRM Y.........
ERalpha       382  WLEILMIGLV WRSME.....  .HPGKLLFAP NL...LLDRN ..Q.GKCVEG MV........
ERbeta        331  WMEVLMMGLM WRSID.....  .HPGKLIFAP DL...VLDRD ..E.GKCVEG IL........
VitDR         216  AIEVIMLRSN ESF...TMD.  ...DMSWTCG N.QDYKYRVS ..D..VT...  ..KAGH....
PPARgamma     322  VHEIIYTMLA SLM...NK..  ...DGVLISE GQ...GFMTR E.F..LK...  ......SLRK
MR            806  WMCLSSFALS WRSYK....H TNSQFLYFAP DL...VFNEE .KM..HQSAM YE........
TRbeta        301  CMEIMSLRAA VRY...DPE.  ..SETLTLNG EM...AVTRG ..Q..LK...  ..NGGL....
GR            600  WMFLMAFALG WRSYR....Q SSANLLCFAP DL...IINEQ .R...MTLPC MY........

RXRalpha      345  ...A.IF.DR VLTELVSKMR DMQMDKTELG CLRAIVL.FN PDSKG...LS  ..........
RARgamma      305  ..GP.LT.DL VFAFAGQLL.  PLEMDDTETG LLSAICL.IC GDRMD...LE  ..........
PR            796  ...S.LC.LT MWQIPQEFV.  KLQVSQEEFL CMKVLLL.LN .TIP.LEGLR  ..........
AR            783  ...S.QC.VR MRHLSQEFG.  WLQITPQEFL CMKALLL.FS .IIP.VDGLK  ..........
ERalpha       422  ...E.IF.DM LLATSSRFR.  MMNLQGEEFV CLKSIILLNS .GV.......  YTF.LSSTLK
ERbeta        371  ...E.IF.DM LLATTSRFR.  ELKLQHKEYL CVKAMILLNS ..........  ...LVTAT.Q
VitDR         255  ..SLELI.EP LIKFQVGLK.  KLNLHEEEHV LLMAICI.VS PDRPG...VQ  ..........
PPARgamma     359  PFGD.FM.EP KFEFAVKFN.  ALELDDSDLA IFIAVII.LS GDRPG...LL  ..........
MR            848  ...L..C.QG MHQISLQFV.  RLQLTFEEYT IMKVLLL.LS .TIP.KDGLK  ..........
TRbeta        339  ..GV.VS.DA IFDLGMSLS.  SFNLDDTEVA LLQAVLL.MS SDRPG...LA  ..........
GR            641  ...D..QCKH MLYVSSELH.  RLQVSYEEYL CMKTLLL.LS .SVP.KDGLK  ..........

RXRalpha      386  ...NPAEVEA LREKVYASLE AYCKH..KYP EQPG......  ...RFAKLLL RLPALRSIGL
RARgamma      336  ...EPEKVDK LQEPLLEALR LYARR..RRP SQPY......  ...MFPRMLM KITDLRGIST
PR            837  ...SQTQFEE MRSSYIRELI KAIG...LRQ K...GVV..S SSQRFYQLTK LLDNLHDLVK
AR            824  ...NQKFFDE LRMNYIKELD RIIA...CKR K...NPT..S CSRRFYQLTK LLDSVQPIAR
ERalpha       467  SLEEKDHIHR VLDKITDTLI HLMA...KAG L...TLQ..Q QHERLAQLLL ILSHIRHMSN
ERbeta        411  DADSSRKLAH LLNAVTDALV WVIA...KSG I...SSQ..Q QSMRLANLLM LLSHVRHASN
VitDR         297  ...DAALIEA IQDRLSNTLQ TYIRC..RHP PP.L......  ...LYAKMIQ KLADLRSLNE
PPARgamma     402  ...NVKPIED IQDNLLQALE LQLKL..NHP ESSQ......  ...LFAKLLQ KMTDLRQIVT
MR            888  ...SQAAFEE MRTNYIKELR KMVT.KCPNN S...G....Q SWQRFYQLTK LLDSMHDLVS
TRbeta        380  ...CVERIEK YQDSFLLAFE HYINY..RKH HVTH......  ...FWPKLLM KVTDLRMIGA
GR            681  ...SQELFDE IRMTYIKELG KAIV...KRE G...N..SSQ NWQRFYQLTK LLDSMHEVVE

RXRalpha      432  KCLEHLFFFK LIGDTPIDTF LMEMLEAPHQ MT........  ..........  ..........
RARgamma      382  KGAERA....  ..........  ..........  ...ITLKMEI PGP....MPP LIREMLENP.
PR            886  QLHLYC....  ..........  ..........  ..........  ..........  .........L
AR            873  ELHQFT....  ..........  ..........  ..........  ..........  .........F
ERalpha       519  KGMEHL....  ..........  ..........  ..........  ..........  .........Y
ERbeta        463  KGMEHL....  ..........  ..........  ..........  ..........  .........L
VitDR         342  EHSKQY....  ..........  ..........  ...RCLSFQP ECSMK..LTP LVLEVFG...
PPARgamma     448  EHVQLL....  ..........  ..........  ..QVIKKTET DMS....LHP LLQEIYKDL.
MR            937  DLLEFC....  ..........  ..........  ..........  ..........  .........F
TRbeta        426  CHASRF....  ..........  ..........  ...LHMKVEC PT...ELFPP LFLEVFE...
GR            730  NLLNYC....  ..........  ..........  ..........  ..........  .........F
```

FIGURE 2 (continued)

```
RXRalpha        .......... .......... .......... .......... .......... ..........
RARgamma        .......... .......... .......... .......... .......... ..........
PR          893 .NTFIQSRAL SVEFPEMMSE VIAAQLPKIL AGMVKPLLFH K......... ..........
AR          880 .DLLIKSHMV SVDFPEMMAE IISVQVPKIL SGKVKPIYFH T......... ..........
ERalpha     526 .SMKCKNV.. .......... .......... .......... .VPLYDLLLE ML........
ERbeta      470 NMKC...... .......... .......... .......... .......... ..KNVVPVYD
VitDR           .......... .......... .......... .......... .......... ..........
PPARgamma       .......... .......... .......... .......... .......... ..........
MR          944 .YTFRESHAL KVEFPAMLVE IISDQLPKVE SGNAKPLYFH R......... ..........
TRbeta          .......... .......... .......... .......... .......... ..........
GR          737 .QTFLDKTMS IEFPEMLAEI ITNQIPKYSN GNIKKLLFHQ K......... ..........

RXRalpha        .......... .....
RARgamma        .......... .....
PR              .......... .....
AR              .......... .....
ERalpha         .......... .....
ERbeta      482 LLLEMLNAHV LR...
VitDR           .......... .....
PPARgamma   477 .......... ..Y..
MR          984 .......... ...K.
TRbeta      453 .......... ....D
GR              .......... .....
```

FIGURE 3

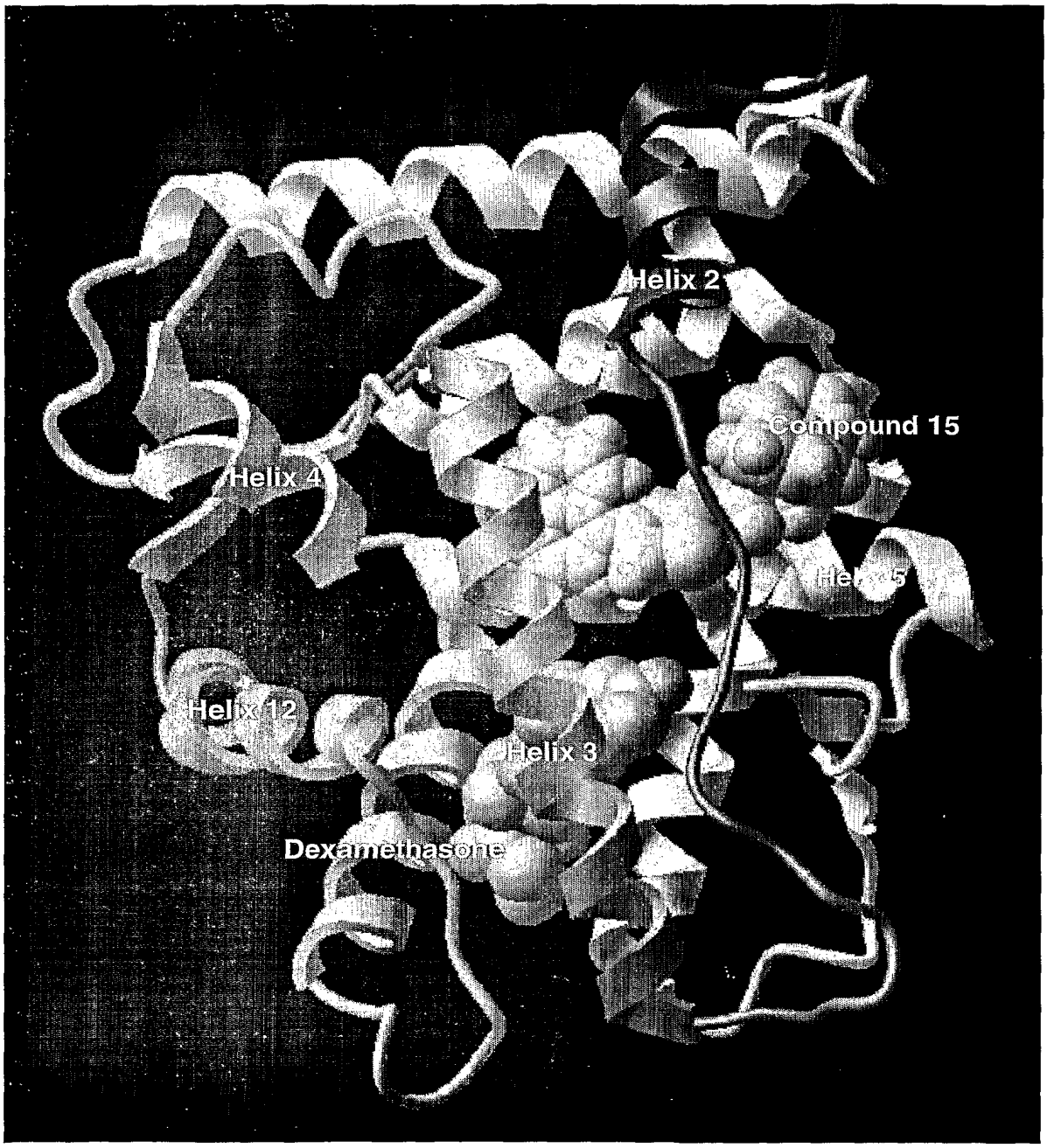
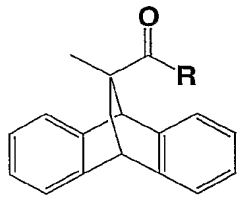


Figure 3.

FIGURE 4



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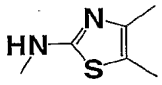
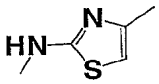
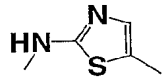
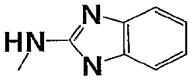
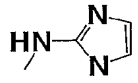
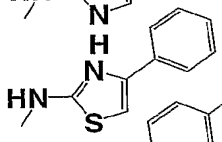
1 

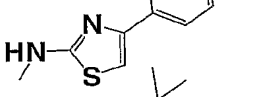
6 

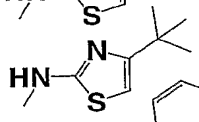
7 

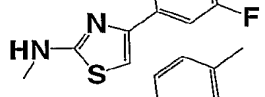
8 

9 

10 

11 

12 

13 

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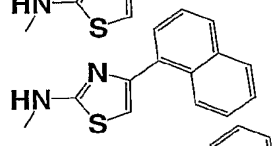
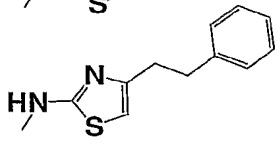
15 

16 

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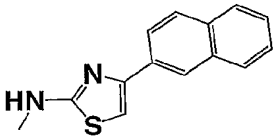
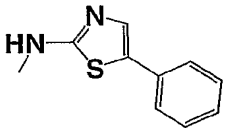
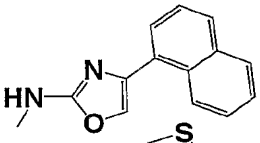
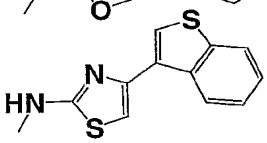
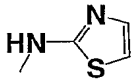
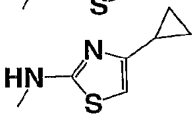
19 

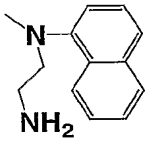
20 

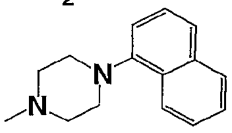
21 

22 

2 

23 

24 

5 

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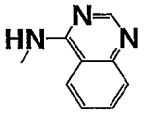
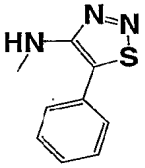
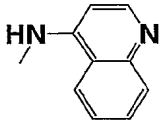
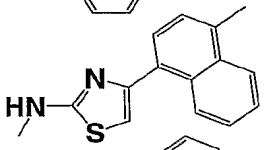
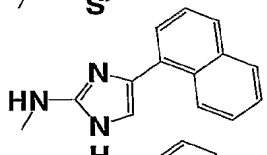
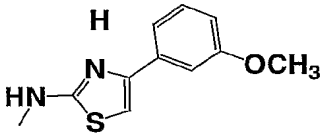
25 

26 

27 

28 

29 

30 

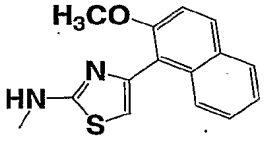
31 

FIGURE 5

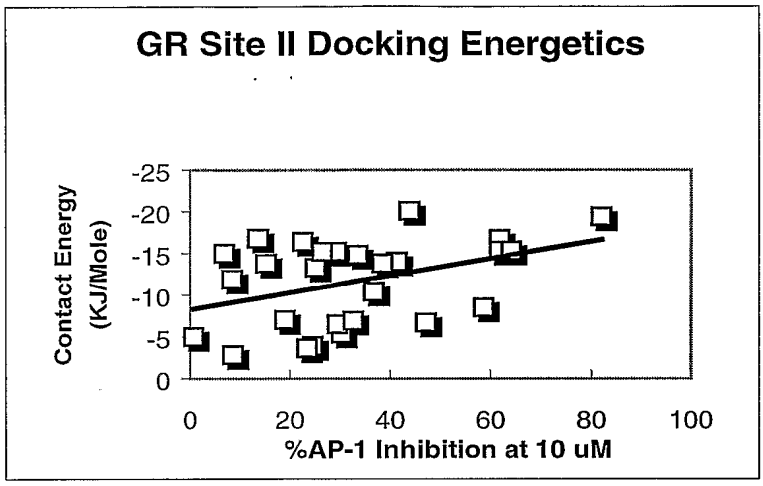

GR Site II Docking Energetics
Contact Energy (KJ/Mole)
-25
-20
-15
-10
-5
0
0
20
40
60
80
100
%AP-1 Inhibition at 10 uM

FIGURE 6

```
u87951 Squirrel     MDSKESLTP. GKEENPSSVL TQERGNVMDF CKILRGGATL KVSVSSTSLA
AF141371 Pig        .......... .......... .......... .......... ..........
l13196 Guinea Pig   MDLKESVTSS ..KEVPSSVL GSERRNVIDF YKTVRGGATV KVSASSPSLA
u87953 Marmoset     MDSKESLTP. GKEENPSSVL TQERGNVMDF CKILRGGATL KVSVSSTSLA
u87952 Ma'z Monkey  MDSKESLTP. GKEENPSSVL TQERGNVMDF SKILRGGATL KVSVSSTSLA
Human               MDSKESLTP. GREENPSSVL AQERGDVMDF YKTLRGGATV KVSASSPSLA
m14053 rat          MDSKESLAPP GRDEVPGSLL GQGRGSVMDF YKSLRGGATV KVSASSPSVA
x04435 mouse        MDSKESLAPP GRDEVPSSLL GRGRGSVMDL YKTLRGGATV KVSASSPSVA

u87951 Squirrel     AASQSDSKQQ RLLVDFPKGS VSNAQQ.... .......... ......PDLS
AF141371 Pig        .......... .VSASSPSLA AVSQPDSKQQ RLAVDFPKGS GSNAQQPDLS
l13196 Guinea Pig   AAAQSDSKQR RLLVDFPKGS GSNAQQ.... .......... ......PDLS
u87953 Marmoset     AASQSDSKQQ RLLVDFPKGS VSNAQQ.... .......... ......PDLS
u87952 Ma'z Monkey  AASQSDSKQQ RLLVDFPKGS VSNAQQ.... .......... ......PDLS
Human               VASQSDSKQR RLLVDFPKGS VSNAQQ.... .......... ......PDLS
m14053 rat          AASQADSKQQ RILLDFSKGS TSNVQQRQQQ QQQQQQQQQQ QQQQQQPGLS
x04435 mouse        AASQADSKQQ RILLDFSKGS ASNAQQ.... ........QQ QQQQPQPDLS

u87951 Squirrel     KAVSLSMGLY MGETETKVMG NDLGFPQQGQ ISLSSGETDL QLLEESIANL
AF141371 Pig        KAVSLSMGLY MGETETKVMG SDLGFPQQGQ ISLSSGETDF RLLEESIANL
l13196 Guinea Pig   KAVSLSMGLY MGETETKVMG NDLGFPQQGQ ISLPSGETDF RLLEESIANL
u87953 Marmoset     KAVSLSMGLY MGETETKVMG NDLGFPQQGQ ISLSSGETDL QLLEESIANL
u87952 Ma'z Monkey  KAVSLSMGLY MGETETKVMG NDLGFPQQGQ ISLSSGETDL QLLEESIANL
Human               KAVSLSMGLY MGETETKVMG NDLGFPQQGQ ISLSSGETDL KLLEESIANL
m14053 rat          KAVSLSMGLY MGETETKVMG NDLGYPQQGQ LGLSSGETDF RLLEESIANL
x04435 mouse        KAVSLSMGLY MGETETKVMG NDLGYPQQGQ LGLSSGETDF RLLEESIANL

u87951 Squirrel     NRSTSVPENP KSSASSSVSA APKEKEFPKT HSDVSSEQQN LKGQTGSNGG
AF141371 Pig        SRSTSVPENP KSSASAAGPA APAEKAFPKT HSDGAPEQPN VKGQTGTNGG
l13196 Guinea Pig   SRSTSVPENP KNSASA.VSG TPTE.EFPKT QSDLSSEQEN LKSQAGTNGG
u87953 Marmoset     NRSTSVPENP KSSASSSVSA APKEKEFPKT HSDVSSEQQN LKGQTGTNGG
u87952 Ma'z Monkey  NRSTSVPENP KSSASSSVSA APKEKEFPKT HSDVSSEQQN LKGQTGTNGG
Human               NRSTSVPENP KSSASTAVSA APTEKEFPKT HSDVSSEQQH LKGQTGTNGG
m14053 rat          NRSTSVPENP KSSTSATGCA TPTEKEFPKT HSDASSEQQN RKSQTGTNGG
x04435 mouse        NRSTSRPENP KSSTPAAGCA TPTEKEFPQT HSDPSSEQQN RKSQPGTNGG

u87951 Squirrel     NVKLYTADQS TFDI....LQ DLEFSSGSPG KETNQSPWKS DLLIDENCLL
AF141371 Pig        NVKLFTTDQS TFDIWRKKLQ DLELPSGSPG KETSESPWSS DLLIDENCLL
l13196 Guinea Pig   NVK.FPPDQS TFDI....LK DLEFSSGSPG KERSESPWRP DLLMDESCLL
u87953 Marmoset     NAKLCTADQS TFDI....LQ DLEFSSGSPG KETNQSPWRS DLLIDENCLL
u87952 Ma'z Monkey  NVKLYTADQS TFDI....LQ DLEFSSGSPG KETNQSPWRS DLLIDENCLL
Human               NVKLYTTDQS TFDI....LQ DLEFSSGSPG KETNESPWRS DLLIDENCLL
m14053 rat          SVKLYPTDQS TFDL....LK DLEFSAGSPS KDTNESPWRS DLLIDEN.LL
x04435 mouse        SVKLYTTDQS TFDI....LQ DLEFSAGSPG KETNESPWRS DLLIDEN.LL
```

FIGURE 6 (Continued)

```
u87951 Squirrel      SPLAGEEDSF LLEGNSNEDC KPLILPDTKP KIKDNGDLVL SSSSNVTLPQ
AF141371 Pig         SPLAGEEDPF LLEGSSTEDC KPLVLPDTKP KVKDNGELIL PSPNSVPLPQ
113196 Guinea Pig    SPLAGEDDPF LLEGNSNEDC KPLILPDTKP KIKDNGDGIL SSSNSVPQPQ
u87953 Marmoset      SPLAGEEDSF LLEGNSNEDC KPLILPDTKP KIKDNGDLVL SSSSNVTLPQ
u87952 Ma'z Monkey   SPLAGEEDSF LLEGNSNEDC KPLILPDTKP KIKDNGDLVL SSSSNVTLPQ
Human                SPLAGEDDSF LLEGNSNEDC KPLILPDTKP KIKDNGDLVL SSPSNVTLPQ
m14053 rat           SPLAGEDDPF LLEGNTNEDC KPLILPDTKP KIKDTGDTIL SSPSSVALPQ
x04435 mouse         SPLAGEDDPF LLEGDVNEDC KPLILPDTKP KIQDTGDTIL SSPSSVALPQ

u87951 Squirrel      VKTEKEDFIE LCTPGVIKQE KLSTVYCQAS FPGANIIGNK MSAISIHGVS
AF141371 Pig         VKTEKEDFIE LCTPGVIKQE KLGPAYCQAS FSGANIIGGK MSAISVHGVS
113196 Guinea Pig    VKIGKEDFIE LCTPGVIKQE KLGPVYCQAS FSGANIIGNK MSAISVHGVS
u87953 Marmoset      VKTEKEDFIE LCTPGVIKQE KLSTVYCQAS FPGANIIGNK MSAISIHGVS
u87952 Ma'z Monkey   VKTEKEDFIE LCTPGVIKQE KLSTVYCQAS FPGANVIGNK MSAISIHGVS
Human                VKTEKEDFIE LCTPGVIKQE KLGTVYCQAS FPGANIIGNK MSAISVHGVS
m14053 rat           VKTEKDDFIE LCTPGVIKQE KLGPVYCQAS FSGTNIIGNK MSAISVHGVS
x04435 mouse         VKTEKDDFIE LCTPGVIKQE KLGPVYCQAS FSGTNIIGNK MSAISVHGVS

u87951 Squirrel      TSGGQMYHYD MNTA.SLSQQ QDQKPIFNVI PPIPVGSENW NRCQGSGDDN
AF141371 Pig         TSGGQLYHYD MNTAASLSKQ QEQKPLFNVI PPIPVGSENW NRCQGSGDDN
113196 Guinea Pig    TSGGQMYHYD MNTA.SLSQQ QDQKPIFNVI PPIPVGSENW NRCQGSGEDN
u87953 Marmoset      TSGGQMYHYD MNTA.SLSQQ QDQKPIFNVI PPIPVGSENW NRCQGSGDDN
u87952 Ma'z Monkey   TSGGQMYHYD MNTA.SLSQQ QDQKPIFNVI PPIPVGSENW NRCQGSGDDN
Human                TSGGQMYHYD MNTA.SLSQQ QDQKPIFNVI PPIPVGSENW NRCQGSGDDN
m14053 rat           TSGGQMYHYD MNTA.SLSQQ QDQKPVFNVI PPIPVGSENW NRCQGSGEDS
x04435 mouse         TSGGQMYHYD MNTA.SLSQQ QDQKPVFNVI PPIPVGSENW NRCQGSGEDN

u87951 Squirrel      LTSLGTLNFP GRTVFSNGYS SPSMRPDVSS PPSSSSTATT GPPPKLCLVC
AF141371 Pig         LTSLGTLNFS GRSVFSNGYS SPGMRPDVSS PPSSSSAAT. GPPPKLCLVC
113196 Guinea Pig    LTSLGTVNFP GRSVFSNGYS SPGLRPDVSS PPSSSST.TT GPPPKLCLVC
u87953 Marmoset      LTSLGTLNFP GRTVFSNGYS SPSMRPDVSS PPSSSSTATT GPPPKLCLVC
u87952 Ma'z Monkey   LTSLGTLNFP GRTVFSNGYS SPSMRPDVSS PPSSSSTATT GPPPKLCLVC
Human                LTSLGTLNFP GRTVFSNGYS SPSMRPDVSS PPSSSSTATT GPPPKLCLVC
m14053 rat           LTSLGALNFP GRSVFSNGYS SPGMRPDVSS PPSSSSAAT. GPPPKLCLVC
x04435 mouse         LTSLGAMNFA GRSVFSNGYS SPGMRPDVSS PPSSSSTAT. GPPPKLCLVC

u87951 Squirrel      SDEASGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
AF141371 Pig         SDEASGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
113196 Guinea Pig    SDELSGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRENCP
u87953 Marmoset      SDEASGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
u87952 Ma'z Monkey   SDEASGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
Human                SDEASGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
m14053 rat           SDEASGCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
x04435 mouse         SDEASVCHYG VLTCGSCKVF FKRAVEGQHN YLCAGRNDCI IDKIRRKNCP
```

FIGURE 6 (Continued)

```
u87951 Squirrel          ACRYRKCLQA GMNLEARKTK KKIKGIQQAT TGVSQETSEN PANKTIVPAT
AF141371 Pig             ACRYRKCLQA GMNLEARKTK KKIKGIQQAT TGVSQETSEN SANKTIVPAT
l13196 Guinea Pig        ACRYRKCLQA GMNLQARKTK KKIKGIQQAT TGVSQNTSEN P.NKTIVPAT
u87953 Marmoset          ACRYRKCLQA GMNLEARKTK KKIKGIQQAT TGVSQETSEN PANKTIVPAT
u87952 Ma'z Monkey       ACRYRKCLQA GMNLEARKTK KKIKGIQQAT TGVSQETSEN PANKTIVPAT
Human                    ACRYRKCLQA GMNLEARKTK KKIKGIQQAT TGVSQETSEN PGNKTIVPAT
m14053 rat               ACRYRKCLQA GMNLEARKTK KKIKGIQQAT AGVSQDTSEN P.NKTIVPAA
x04435 mouse             ACRYRKCLQA GMNLEARKTK KKIKGIQQAT AGVSQDTSEN .ANKTIVPAA

u87951 Squirrel      525 LPQLTPTLVS LLEVIEPEVL YAGYDSTVPD STWRIMTTLN MLGGRQVIAA
AF141371 Pig         489 LPQLTPTLVS LLEVIEPEVL YAGYDSSIPD STWRIMTALN MLGGRQVIAA
l13196 Guinea Pig    519 LPQLTPTLVS LLEVIEPEVI HSGYDSTSPD STWRIMTTLN MLGGRQVIAA
u87953 Marmoset      525 LPQLTPTLVS LLEVIEPEVL YAGYDSTVPD STWRIMTTLN MLGGRQVIAA
u87952 Ma'z Monkey   525 LPQLTPTLVS LLEVIEPEVL YAGYDSTVPD STWRIMTTLN MLGGRQVIAA
Human                525 LPQLTPTLVS LLEVIEPEVL YAGYDSSVPD STWRIMTTLN MLGGRQVIAA
m14053 rat           543 LPQLTPTLVS LLEVIEPEVL YAGYDSSVPD SAWRIMTTLN MLGGRQVIAA
x04435 mouse         531 LPQLTPTLVS LLEVIEPEVL YAGYDSSVPD SAWRIMTTLN MLGGRQVIAA

u87951 Squirrel      575 VKWAKAIPGF RNLHLDDQMT LLQYSWMFLM AFALGWRSYR QASSNLLCFA
AF141371 Pig         539 VKWAKAIPGF RNLHLDDQMT LLQYSWMFLM VFALGWRSYR QSSASLLCFA
l13196 Guinea Pig    569 VKWAKAIPGF KNLHLDDQMT LLQYSWMFLM AFALGWRSYK QSNGSLLCFA
u87953 Marmoset      575 VKWAKAIPGF RNLHLDDQMT LLQYSWMFLM AFALGWRSYR QASSNLLCFA
u87952 Ma'z Monkey   575 VKWAKAIPGF RNLHLDDQMT LLQYSWMFLM AFALGWRSYR QASSNLLCFA
Human                575 VKWAKAIPGF RNLHLDDQMT LLQYSWMFLM AFALGWRSYR QSSANLLCFA
m14053 rat           593 VKWAKAILGL RNLHLDDQMT LLQYSWMFLM AFALGWRSYR QSSGNLLCFA
x04435 mouse         581 VKWAKAIPGF RNLHLDDQMT LLQYSWMFLM AFALGWRSYR QASGNLLCFA

u87951 Squirrel      625 PDLIINEQRM TLPCMYDQCK HMLYVSSELH RLQVSYEEYL CMKTLLLLSS
AF141371 Pig         589 PDLVINEQRM ALPCMYDQCR HMLYVSSELQ RLQVSYEEYL CMKTLLLLSS
l13196 Guinea Pig    619 PDLIINEQRM SLPWMYDQCR YMLYVSSELK RLQVSYEEYL CMKTLLLLSS
u87953 Marmoset      625 PDLIINEQRM TLPCMYDQCK HMLYVSSELH RLQVSYEEYL CMKTLLLLSS
u87952 Ma'z Monkey   625 PDLIINEQRM TLPCMYDQCK HMLYVSSELH RLQVSYEEYL CMKTLLLLSS
Human                625 PDLIINEQRM TLPCMYDQCK HMLYVSSELH RLQVSYEEYL CMKTLLLLSS
m14053 rat           643 PDLIINEQRM SLPCMYDQCK HMLFVSSELQ RLQVSYEEYL CMKTLLLLSS
x04435 mouse         631 PDLIINEQRM TLPCMYDQCK HMLFISTELQ RLQVSYEEYL CMKTLLLLSS

u87951 Squirrel          VPKDGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
AF141371 Pig             VPKDGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
l13196 Guinea Pig        VPKEGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
u87953 Marmoset          VPKDGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
u87952 Ma'z Monkey       VPKDGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
Human                    VPKDGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
m14053 rat               VPKEGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
x04435 mouse             VPKEGLKSQE LFDEIRMTYI KELGKAIVKR EGNSSQNWQR FYQLTKLLDS
                     675
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FIGURE 6 (Continued)

```
u87951 Squirrel          MHEVVENLLN YCFQTFLDKT MSIEFPEMLA EIITNQLPKY SNGNIKKLLF
AF141371 Pig             MHDVVENLLN YCFQT..... .......... .......... ..........
l13196 Guinea Pig        LHEIVGNLLN ICFKTFLDKT MNIEFPEMLA EIITNQLPKY SNGDIKKLLF
u87953 Marmoset          MHEVVENLLN YCFQTFLDKT MSIEFPEMLA EIITNQLPKY SNGNIRKLLF
u87952 Ma'z Monkey       MHEVVENLLN YCFQTFLDKT MSIEFPEMLA EIITNQLPKY SNGNIKKLLF
Human                    MHEVVENLLN YCFQTFLDKT MSIEFPEMLA EIITNQIPKY SNGNIKKLLF
m14053 rat               MHEVVENLLT YCFQTFLDKT MSIEFPEMLA EIITNQIPKY SNGNIKKLLF
x04435 mouse             MHDVVENLLS YCFQTFLDKS MSIEFPEMLA EIITNQIPKY SNGNIKKLLF

u87951 Squirrel          HQK
AF141371 Pig             ...
l13196 Guinea Pig        HQK
u87953 Marmoset          HQK
u87952 Ma'z Monkey       HQK
Human                    HQK
m14053 rat               HQK
x04435 mouse             HQK
```

FIGURE 7

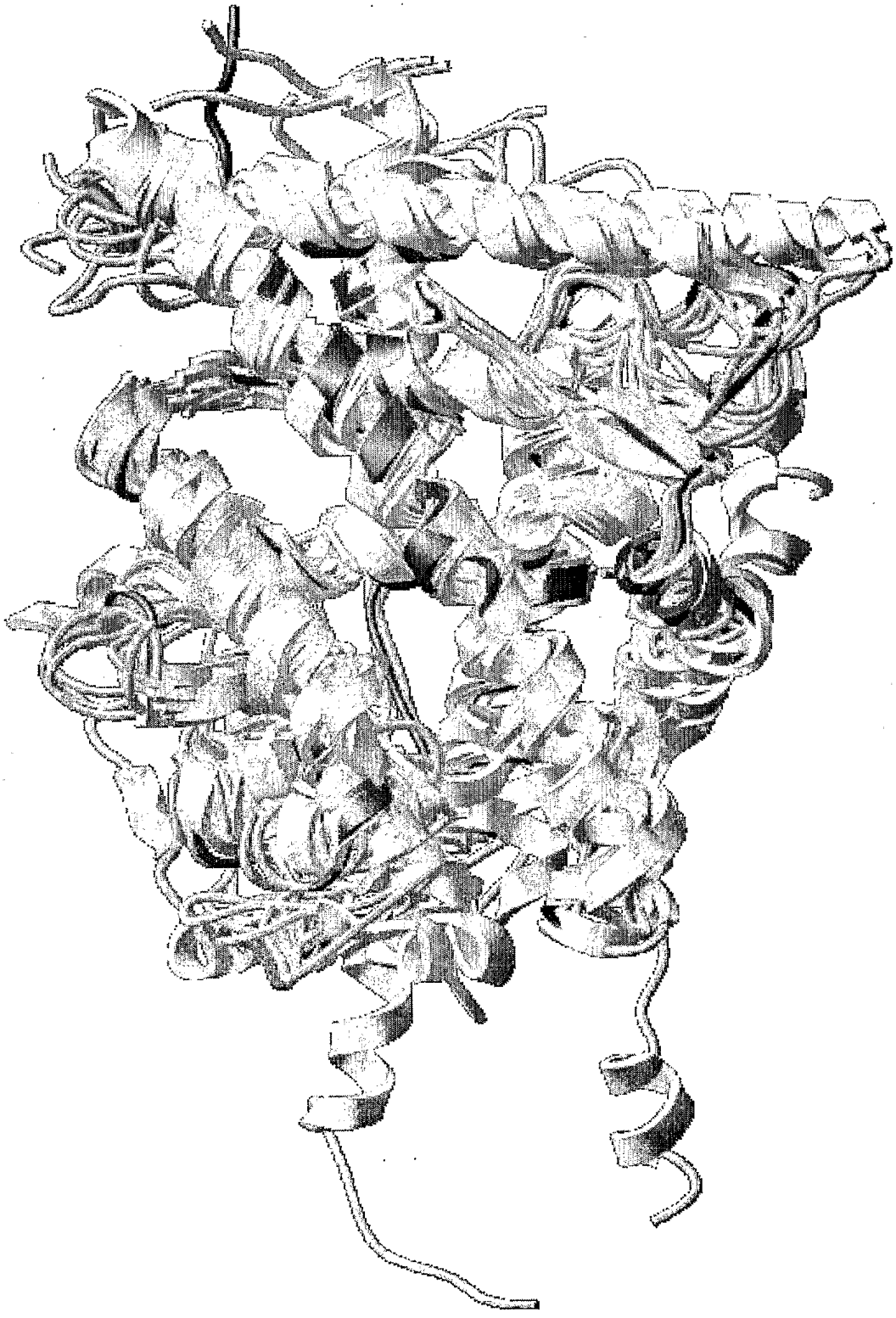


FIGURE 8

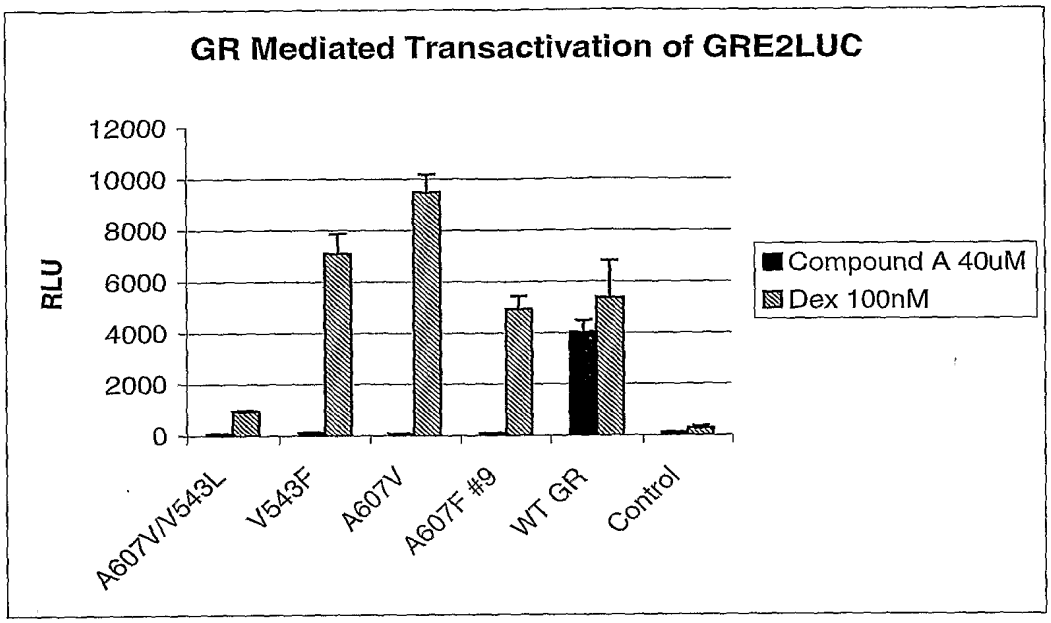

GR Mediated Transactivation of GRE2LUC
RLU
12000
10000
8000
6000
4000
2000
0
A607V/V543L
V543F
A607V
A607F #9
WT GR
Control
Compound A 40uM
Dex 100nM

FIGURE 9

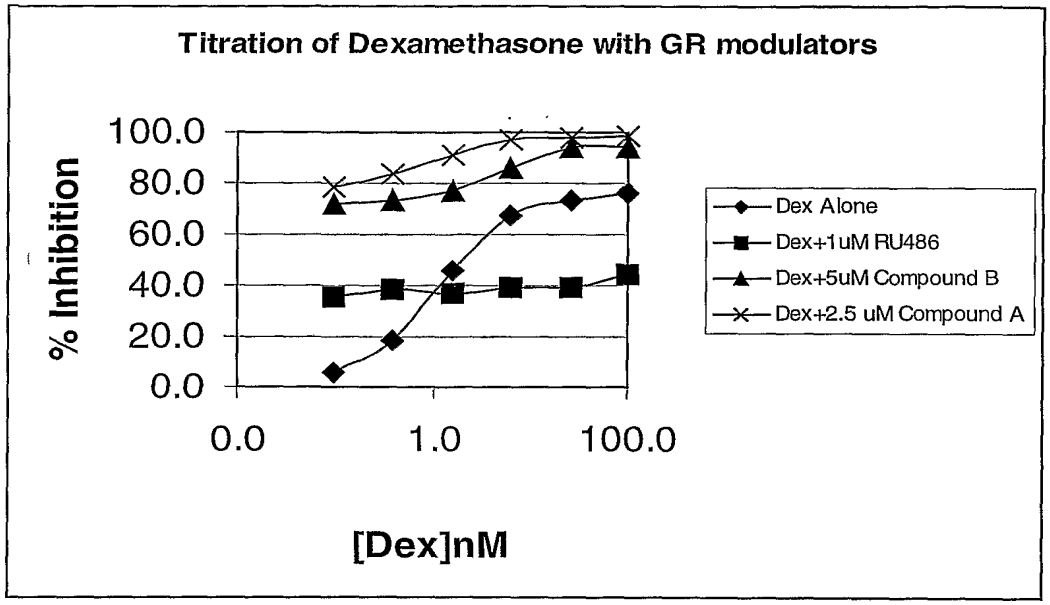

Titration of Dexamethasone with GR modulators
% Inhibition
100.0
80.0
60.0
40.0
20.0
0.0
0.0
1.0
100.0
[Dex]nM
Dex Alone
Dex+1uM RU486
Dex+5uM Compound B
Dex+2.5 uM Compound A

FIGURE 10

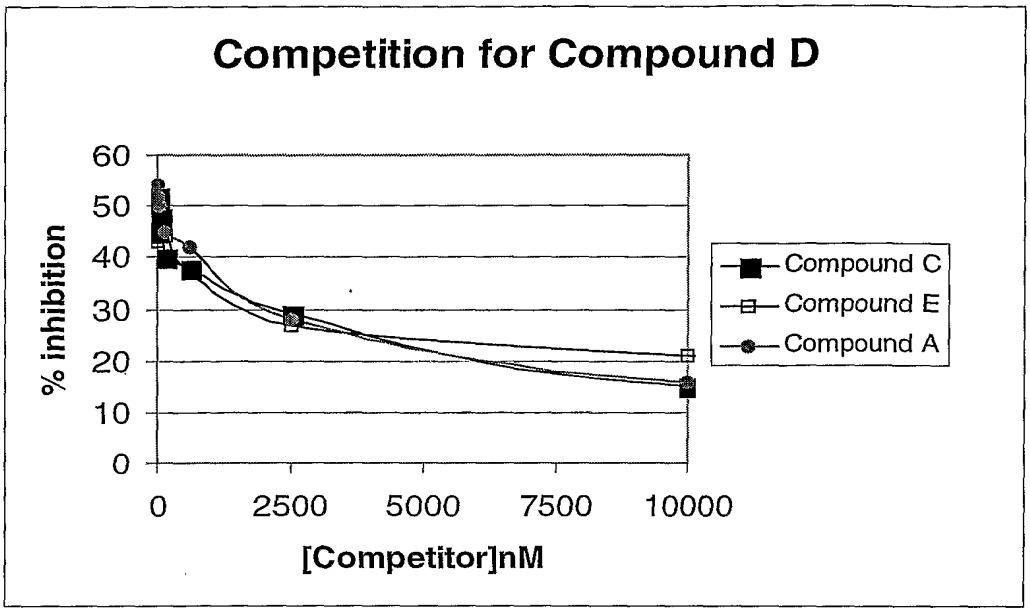

Competition for Compound D
% inhibition
60
50
40
30
20
10
0
0
2500
5000
7500
10000
[Competitor]nM
Compound C
Compound E
Compound A

FIGURE 11a

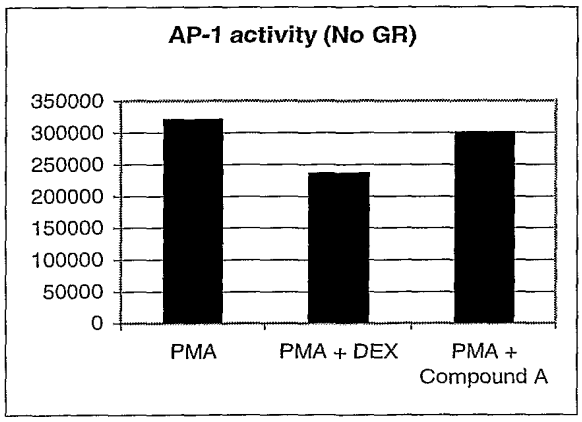
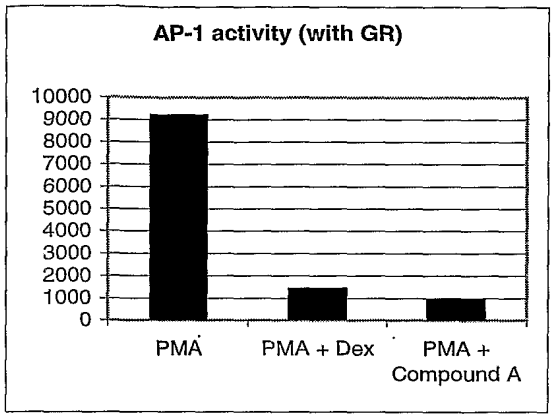


FIGURE 11b



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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: COMPOSITIONS AND METHODS INVOLVING NUCLEAR HORMONE RECEPTOR SITE II

(57) Abstract: A binding site in nuclear hormone receptors is described and its structural coordinates are provided. The invention provides machine-readable data storage media comprising structure coordinates of Site II and computer systems comprising the machine-readable data storage media. The invention provides methods used in the design and identification of ligands of Site II and of modulators of nuclear hormone receptors. The invention provides ligands of Site II, modulators of NHRs, pharmaceutical compositions comprising modulators of NHRs, methods of modulating NHRs, and methods of treating diseases by administering modulators of an NHR. Also provided are methods of designing mutants, mutant NHRs, Site II binding assays, and models of Site II.

WO 2004/009016 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/22299

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : G06F 19/00

US CL : 702/27

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 702/27, 530/350, 358, 412, 418

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WEST: USP, PGPub, EUPA, JAPA, and WPID; STN:Medline, CaPlus, Scisearch, Lifesci, Bioses, and Embase.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BLEDSOE et al. Crystal structure of the glucocorticoid receptor ligand binding domain reveals a novel mode of receptor dimerization and coactivator recognition. Cell. 12 July 2002, Vol. 110, pages 93-105, see abstract.	1-29
Y,P	KAUPPI et al. The three-dimensional structure of antagonistic and agonistic forms of the glucocorticoid receptor ligand-binding domain: RU-486 induces a transconformation that leads to active antagonism. J. Biol. Chem. 20 June 2003, Vol. 278, No. 25, pages 22748-22754, see abstract.	1-29
Y	DEY et al. Homology modelling of the ligand-binding domain of glucocorticoid receptor: binding site interactions with cortisol and corticosterone. Protein Engineering. 2001, Vol. 14, No. 8, pages 565-571, see abstract.	1-29
A	AGIUS et al. Identification of glucocorticoid receptor in the human leukemia cell line K562. J. Lab. Clin. Med. August 1982, Vol. 100, No. 2, pages 178-185, see abstract.	1-29
Y	HOLLENBERG et al. Primary structure and expression of functional human glucocorticoid receptor cDNA. Nature. 26 December 1985, Vol. 318, pages 635-641, see abstract.	1-29
Y	US 5,759,785 A (TSAI et al.) 02 June 1998, see abstract.	1-29

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

23 June 2005 (23.06.2005)

Date of mailing of the international search report

19 AUG 2005

Name and mailing address of the ISA/US

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Form PCT/ISA/210 (second sheet) (July 1998)

PCT/US03/22299

INTERNATIONAL SEARCH REPORT

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BAUMANN et al. Refined solution structure of the glucocorticoid receptor DNA-binding domain. Biochemistry. 1993, Vol. 32, 13463-13471, see abstract.	1-29
Y	WURTZ et al. Three-dimensional models of estrogen receptor ligand binding domain complexes, based on related crystal structures and mutational and structure-activity relationship data. J. Med. Chem. 1998, Vol. 41, pages 1803-1814, see abstract.	1-29
Y	WO 00/52050 A2 (KARO BIO AB) 08 September 2000, see abstract.	1-29
Y,P	WO 03/015692 A2 (SMITHKLINE BEECHAM CORPORATION) 27 February, 2003, see the entire document.	1-29
Y	GOLDSTEIN et al. Three-dimensional model for the hormone binding domains of steroid receptor. Proc. Natl. Acad. Sci. USA November 1993, Vol. 90, pages 9949-9953, see abstract.	1-29
Y	MAKINO et al. Automated flexible ligand docking method and its application for database search. J. Comput. Chem. 1997, Vol. 18, No. 14, pages 1812-1825, see abstract.	1-29
Y	TAPIA et al. Computer assisted simulation and molecular graphics methods in molecular design: 1. Theory and Applications to Enzyme Active-Site Directed Drug Design. Mol. Engin. 1994, Vol. 3, pages 377-414, see the abstract.	1-29
Y	US 6,236,946 B1 (SCANLAN et al.) 22 May 2001, see abstract.	1-29

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US03/22299

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claim Nos.: 30-36
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Please See Continuation Sheet

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-29

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Continuation of Box I Reason 2:
The claims are directed to any chemical compound which can binds to NHR site II and their use in modulating NHR activity and any treating diseases. The claim does not define any structural element which would allow a proper search for the claims.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-29, drawn to a method of evaluating chemical entity to bind nuclear hormone receptor (NHR) site II.

Group II, claim(s) 37, drawn to a mutant of NHR comprising one or more amino acid mutation in site II.

Group III, claim(s) 38 and 39, drawn to a method of measuring the binding of a test compound to NHR site II.

The inventions listed as Groups I-III do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The special technical feature for the invention of Group I is the algorithm that allow identification of compound that binds or interact with NHR site II, whereas the special technical feature for the invention of Group II is the algorithm that is capable of identifying mutants NHR. The special technical feature of the invention of Group III is the NHR, which differs from those of Groups I and II. Thus, the claimed inventions lack special technical feature. Claims 30-36 are unsearchable because they are directed to any chemical compound which binds to NHR site II. The claims do not define a structural element by which the claim can be searched.